GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 08:47:48 ; Search time 1 Seconds
(without alignments)
5.870 Million cell updates/sec

Title: us-09-402-569-4
Perfect score: 1443
Sequence: 1 atgtctgctgaagtcatcca.....ttatcctctcctacacataa 1443

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 2034 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : us-09-009-893a-1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1441.4	99.9	2034	1	us-09-009-893a-1	
c 2	25.2	1.7	2034	1	us-09-009-893a-1	

ALIGNMENTS

RESULT 1
us-09-009-893a-1

Query Match 99.9%; Score 1441.4; DB 1; Length 2034;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ATGTCTGCTGAAGTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGGAGATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 ATGTCTGCTGAAGTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGGAGATG 327

Qy         61 CTGCTCTTTTTGTGCCGGGATGTTGCTATAGATGTGGTTCCACCTAATGTCAGGGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 CTGCTCTTTTTGTGCCGGGATGTTGCTATAGATGTGGTTCCACCTAATGTCAGGGACCTT 387

Qy        121 CTGGATATTTTACGGGAAAGAGGTAAGCTGTCTGTCGGGGACTTGGCTGAACTGCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 CTGGATATTTTACGGGAAAGAGGTAAGCTGTCTGTCGGGGACTTGGCTGAACTGCTCTAC 447

Qy        181 AGAGTGAGGCGATTTGACCTGCTCAAACGTATCTTGAAGATGGACAGAAAAGCTGTGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 AGAGTGAGGCGATTTGACCTGCTCAAACGTATCTTGAAGATGGACAGAAAAGCTGTGGAG 507

Qy        241 ACCCACCTGCTCAGGAACCCTCACCTTGTTTCGGACTATAGAGTGCTGATGGCAGAGATT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 ACCCACCTGCTCAGGAACCCTCACCTTGTTTCGGACTATAGAGTGCTGATGGCAGAGATT 567

Qy        301 GGTGAGGATTTGGATAAATCTGATGTGTCCTCATTAATTTTCCTCATGAAGGATTACATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 GGTGAGGATTTGGATAAATCTGATGTGTCCTCATTAATTTTCCTCATGAAGGATTACATG 627

Qy        361 GGCCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTTGTGGTTGAGTTGGAGAAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 GGCCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTTGTGGTTGAGTTGGAGAAA 687

Qy        421 CTAAATCTGGTTGCCCCAGATCAACTGGATTTATTAGAAAAATGCCTAAAGAACATCCAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 CTAAATCTGGTTGCCCCAGATCAACTGGATTTATTAGAAAAATGCCTAAAGAACATCCAC 747

Qy        481 AGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGCAGGGACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 AGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGCAGGGACA 807

Qy        541 AGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 AGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAAATAAC 867

Qy        601 TTCAGGCTCCATAATGGGAGAAGTAAAGAACAAAGACTTAAGGAACAGCTTGGCGCTCAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        868 TTCAGGCTCCATAATGGGAGAAGTAAAGAACAAAGACTTAAGGAACAGCTTGGCGCTCAA 927

Qy        661 CAAGAACCAGTGAAGAAATCCATTCAGGAATCAGAAGCTTTTTTGCCTCAGAGCATACCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 CAAGAACCAGTGAAGAAATCCATTCAGGAATCAGAAGCTTTTTTGCCTCAGAGCATACCT 987

Qy        721 GAAGAGAGATACAAGATGAAGAGCAAGCCCCTAGGAATCTGCCTGATAATCGATTGCATT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 GAAGAGAGATACAAGATGAAGAGCAAGCCCCTAGGAATCTGCCTGATAATCGATTGCATT 1047

Qy        781 GGCAATGAGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATGAAGTCCAGAAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1048 GGCAATGAGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATGAAGTCCAGAAA 1107

Qy        841 TTCTTGCATCTCAGTATGCATGGTATATCCCAGATTCTTGGCCAATTTGCCTGTATGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1108 TTCTTGCATCTCAGTATGCATGGTATATCCCAGATTCTTGGCCAATTTGCCTGTATGCCC 1167

Qy        901 GAGCACCGAGACTACGACAGCTTTGTGTGTGTCCTGGTGAGCCGAGGAGGCTCCCAGAGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 GAGCACCGAGACTACGACAGCTTTGTGTGTGTCCTGGTGAGCCGAGGAGGCTCCCAGAGT 1227

Qy        961 GTGTATGGTGTGGATCAGACTCACTCAGGGCTCCCCCTGCATCACATCAGGAGGATGTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1228 GTGTATGGTGTGGATCAGACTCACTCAGGGCTCCCCCTGCATCACATCAGGAGGATGTTC 1287

Qy       1021 ATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCCAAAGATGTTTTTTATTCAGAACTAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1288 ATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCCAAAGATGTTTTTTATTCAGAACTAT 1347

Qy       1081 GTGGTGTCAGAGGGCCAGCTGGAGGACAGCAGCCTCTTGGAGGTGGATGGGCCAGCGATG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1348 GTGGTGTCAGAGGGCCAGCTGGAGGACAGCAGCCTCTTGGAGGTGGATGGGCCAGCGATG 1407

Qy       1141 AAGAATGTGGAATTCAAGGCTCAGAAGCGAGGGCTGTGCACAGTTCACCGAGAAGCTGAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1408 AAGAATGTGGAATTCAAGGCTCAGAAGCGAGGGCTGTGCACAGTTCACCGAGAAGCTGAC 1467

Qy       1201 TTCTTCTGGAGCCTGTGTACTGCGGACATGTCCCTGCTGGAGCAGTCTCACAGCTCACCA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1468 TTCTTCTGGAGCCTGTGTACTGCGGACATGTCCCTGCTGGAGCAGTCTCACAGCTCACCG 1527

Qy       1261 TCCCTGTACCTGCAGTGCCTCTCCCAGAAACTGAGACAAGAAAGAAAACGCCCACTCCTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1528 TCCCTGTACCTGCAGTGCCTCTCCCAGAAACTGAGACAAGAAAGAAAACGCCCACTCCTG 1587

Qy       1321 GATCTTCACATTGAACTCAATGGCTACATGTATGATTGGAACAGCAGAGTTTCTGCCAAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1588 GATCTTCACATTGAACTCAATGGCTACATGTATGATTGGAACAGCAGAGTTTCTGCCAAG 1647
```

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Qy       1381 GAGAAATATTATGTCTGGCTGCAGCACACTCTGAGAAAGAAACTTATCCTCTCCTACACA 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1648 GAGAAATATTATGTCTGGCTGCAGCACACTCTGAGAAAGAAACTTATCCTCTCCTACACA 1707

Qy       1441 TAA 1443
              |||
Db       1708 TAA 1710
```

RESULT 2
us-09-009-893a-1/c

Query Match 1.7%; Score 25.2; DB 1; Length 2034;
Best Local Similarity 66.7%; Pred. No. 0;
Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```
Qy        945 AGGAGGCTCCCAGAGTGTGTATGGTGTGGATCAGACTCACTCAGGGCTCCCCCT 998
              ||| ||  ||| ||||| || || |    | || || ||||| |||  || |||
Db       1265 AGGGGGAGCCCTGAGTGAGTCTGATCCACACCATACACACTCTGGGAGCCTCCT 1212
```

Search completed: September 30, 2005, 08:47:50
Job time : 2 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 08:46:37 ; Search time 1 Seconds
(without alignments)
5.902 Million cell updates/sec

Title: us-09-402-569-4
Perfect score: 1443
Sequence: 1 atgtctgctgaagtcatcca.....ttatcctctcctacacataa 1443

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 2045 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : us-08-795-088a-1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1441.4	99.9	2045	1	us-08-795-088a-1	
c 2	25.2	1.7	2045	1	us-08-795-088a-1	

ALIGNMENTS

RESULT 1
us-08-795-088a-1

Query Match 99.9%; Score 1441.4; DB 1; Length 2045;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ATGTCTGCTGAAGTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGGAGATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATGTCTGCTGAAGTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGGAGATG 570

Qy         61 CTGCTCTTTTTGTGCCGGGATGTTGCTATAGATGTGGTTCCACCTAATGTCAGGGACCTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 CTGCTCTTTTTGTGCCGGGATGTTGCTATAGATGTGGTTCCACCTAATGTCAGGGACCTT 630

Qy        121 CTGGATATTTTACGGGAAAGAGGTAAGCTGTCTGTCGGGGACTTGGCTGAACTGCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 CTGGATATTTTACGGGAAAGAGGTAAGCTGTCTGTCGGGGACTTGGCTGAACTGCTCTAC 690

Qy        181 AGAGTGAGGCGATTTGACCTGCTCAAACGTATCTTGAAGATGGACAGAAAAGCTGTGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 AGAGTGAGGCGATTTGACCTGCTCAAACGTATCTTGAAGATGGACAGAAAAGCTGTGGAG 750

Qy        241 ACCCACCTGCTCAGGAACCCTCACCTTGTTTCGGACTATAGAGTGCTGATGGCAGAGATT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 ACCCACCTGCTCAGGAACCCTCACCTTGTTTCGGACTATAGAGTGCTGATGGCAGAGATT 810

Qy        301 GGTGAGGATTTGGATAAATCTGATGTGTCCTCATTAATTTTCCTCATGAAGGATTACATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 GGTGAGGATTTGGATAAATCTGATGTGTCCTCATTAATTTTCCTCATGAAGGATTACATG 870

Qy        361 GGCCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTTGTGGTTGAGTTGGAGAAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 GGCCGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTTGTGGTTGAGTTGGAGAAA 930

Qy        421 CTAAATCTGGTTGCCCCAGATCAACTGGATTTATTAGAAAAATGCCTAAAGAACATCCAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 CTAAATCTGGTTGCCCCAGATCAACTGGATTTATTAGAAAAATGCCTAAAGAACATCCAC 990

Qy        481 AGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGCAGGGACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 AGAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGCAGGGACA 1050

Qy        541 AGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 AGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAAATAAC 1110

Qy        601 TTCAGGCTCCATAATGGGAGAAGTAAAGAACAAAGACTTAAGGAACAGCTTGGCGCTCAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 TTCAGGCTCCATAATGGGAGAAGTAAAGAACAAAGACTTAAGGAACAGCTTGGCGCTCAA 1170

Qy        661 CAAGAACCAGTGAAGAAATCCATTCAGGAATCAGAAGCTTTTTTGCCTCAGAGCATACCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 CAAGAACCAGTGAAGAAATCCATTCAGGAATCAGAAGCTTTTTTGCCTCAGAGCATACCT 1230

Qy        721 GAAGAGAGATACAAGATGAAGAGCAAGCCCCTAGGAATCTGCCTGATAATCGATTGCATT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 GAAGAGAGATACAAGATGAAGAGCAAGCCCCTAGGAATCTGCCTGATAATCGATTGCATT 1290

Qy        781 GGCAATGAGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATGAAGTCCAGAAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 GGCAATGAGACAGAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATGAAGTCCAGAAA 1350

Qy        841 TTCTTGCATCTCAGTATGCATGGTATATCCCAGATTCTTGGCCAATTTGCCTGTATGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 TTCTTGCATCTCAGTATGCATGGTATATCCCAGATTCTTGGCCAATTTGCCTGTATGCCC 1410

Qy        901 GAGCACCGAGACTACGACAGCTTTGTGTGTGTCCTGGTGAGCCGAGGAGGCTCCCAGAGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 GAGCACCGAGACTACGACAGCTTTGTGTGTGTCCTGGTGAGCCGAGGAGGCTCCCAGAGT 1470

Qy        961 GTGTATGGTGTGGATCAGACTCACTCAGGGCTCCCCCTGCATCACATCAGGAGGATGTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 GTGTATGGTGTGGATCAGACTCACTCAGGGCTCCCCCTGCATCACATCAGGAGGATGTTC 1530

Qy       1021 ATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCCAAAGATGTTTTTTATTCAGAACTAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 ATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCCAAAGATGTTTTTTATTCAGAACTAT 1590

Qy       1081 GTGGTGTCAGAGGGCCAGCTGGAGGACAGCAGCCTCTTGGAGGTGGATGGGCCAGCGATG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1591 GTGGTGTCAGAGGGCCAGCTGGAGGACAGCAGCCTCTTGGAGGTGGATGGGCCAGCGATG 1650

Qy       1141 AAGAATGTGGAATTCAAGGCTCAGAAGCGAGGGCTGTGCACAGTTCACCGAGAAGCTGAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1651 AAGAATGTGGAATTCAAGGCTCAGAAGCGAGGGCTGTGCACAGTTCACCGAGAAGCTGAC 1710

Qy       1201 TTCTTCTGGAGCCTGTGTACTGCGGACATGTCCCTGCTGGAGCAGTCTCACAGCTCACCA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1711 TTCTTCTGGAGCCTGTGTACTGCGGACATGTCCCTGCTGGAGCAGTCTCACAGCTCACCG 1770

Qy       1261 TCCCTGTACCTGCAGTGCCTCTCCCAGAAACTGAGACAAGAAAGAAAACGCCCACTCCTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1771 TCCCTGTACCTGCAGTGCCTCTCCCAGAAACTGAGACAAGAAAGAAAACGCCCACTCCTG 1830

Qy       1321 GATCTTCACATTGAACTCAATGGCTACATGTATGATTGGAACAGCAGAGTTTCTGCCAAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1831 GATCTTCACATTGAACTCAATGGCTACATGTATGATTGGAACAGCAGAGTTTCTGCCAAG 1890
```

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Qy       1381 GAGAAATATTATGTCTGGCTGCAGCACACTCTGAGAAAGAAACTTATCCTCTCCTACACA 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1891 GAGAAATATTATGTCTGGCTGCAGCACACTCTGAGAAAGAAACTTATCCTCTCCTACACA 1950

Qy       1441 TAA 1443
             |||
Db       1951 TAA 1953
```

RESULT 2
us-08-795-088a-1/c

Query Match 1.7%; Score 25.2; DB 1; Length 2045;
Best Local Similarity 66.7%; Pred. No. 0;
Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```
Qy        945 AGGAGGCTCCCAGAGTGTGTATGGTGTGGATCAGACTCACTCAGGGCTCCCCCT 998
              ||| ||  ||| ||||| || || |    | || || ||||| |||  || |||
Db       1508 AGGGGGAGCCCTGAGTGAGTCTGATCCACACCATACACACTCTGGGAGCCTCCT 1455
```

Search completed: September 30, 2005, 08:46:39
Job time : 1 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 30, 2005, 08:45:06 ; Search time 0.001 Seconds
(without alignments)
230.400 Million cell updates/sec

Title: us-09-402-569-5
Perfect score: 2470
Sequence: 1 MSAEVIHQVEEALDTDEKEM.....EKYYVWLQHTLRKKLILSYT 480

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 480 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : us-09-009-893a-2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2454	99.4	480	1	us-09-009-893a-2	

ALIGNMENTS

RESULT 1
us-09-009-893a-2

Query Match 99.4%; Score 2454; DB 1; Length 480;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 477; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120

Qy        121 GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLGKCLKNIHRIDLKTKIQKYKQSVQGAGT 180
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        121 GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKYKQSVQGAGT 180

Qy        181 SYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLGAQQEPVKKSIQESEAFLPQSIP 240

Qy        241 EERYKMKSKPLGICLIISCIGNETELLRSTFTSLGYEVQKFLHLSMHGISQILGQFACMP 300
              |||||||||||||||| |||||||||| ||||||||||||||||||||||||||||||||
Db        241 EERYKMKSKPLGICLIIDCIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMP 300

Qy        301 EHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNY 360

Qy        361 VVSEGQLEDSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VVSEGQLEDSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSP 420

Qy        421 SLYLQCLSQKLRQERKRPLLDLHIELNGYMYDWNSRVSAKEKYYVWLQHTLRKKLILSYT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SLYLQCLSQKLRQERKRPLLDLHIELNGYMYDWNSRVSAKEKYYVWLQHTLRKKLILSYT 480
```

Search completed: September 30, 2005, 08:45:06
Job time : 0.001 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 30, 2005, 08:44:29 ; Search time 0.001 Seconds
(without alignments)
230.400 Million cell updates/sec

Title: us-09-402-569-5
Perfect score: 2470
Sequence: 1 MSAEVIHQVEEALDTDEKEM.....EKYYVWLQHTLRKKLILSYT 480

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 480 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : us-08-795-088a-2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2454	99.4	480	1	us-08-795-088a-2	

ALIGNMENTS

RESULT 1
us-08-795-088a-2

Query Match 99.4%; Score 2454; DB 1; Length 480;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 477; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIFLMKDYM 120

Qy        121 GRGKISKEKSFLDLVVELEKLNLVAPDQLDLLGKCLKNIHRIDLKTKIQKYKQSVQGAGT 180
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Qy        301 EHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRMFMGDSCPYLAGKPKMFFIQNY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 VVSEGQLEDSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VVSEGQLEDSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLEQSHSSP 420

Qy        421 SLYLQCLSQKLRQERKRPLLDLHIELNGYMYDWNSRVSAKEKYYVWLQHTLRKKLILSYT 480
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Db        421 SLYLQCLSQKLRQERKRPLLDLHIELNGYMYDWNSRVSAKEKYYVWLQHTLRKKLILSYT 480
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Search completed: September 30, 2005, 08:44:29
Job time : 0.001 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 30, 2005, 07:58:49 ; Search time 42 Seconds
(without alignments)
186.623 Million cell updates/sec

Title: US-09-402-569-2
Perfect score: 521
Sequence: 1 KSRMSAEVIHQVEEALDTDE.....LLRNPHLVSDYRVLMSEIGE 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	504	96.7	221	3	US-09-382-155-17	Sequence 17, Appl
2	504	96.7	221	3	US-09-074-044A-17	Sequence 17, Appl
3	504	96.7	445	3	US-08-859-167-2	Sequence 2, Appli
4	504	96.7	445	3	US-09-109-273-2	Sequence 2, Appli
5	504	96.7	445	3	US-09-276-993-2	Sequence 2, Appli
6	504	96.7	445	4	US-09-723-450-2	Sequence 2, Appli
7	504	96.7	480	3	US-08-795-088A-2	Sequence 2, Appli
8	504	96.7	480	3	US-09-069-023-34	Sequence 34, Appl
9	504	96.7	480	4	US-09-009-893A-2	Sequence 2, Appli
10	504	96.7	480	4	US-09-489-155-2	Sequence 2, Appli
11	384	73.7	78	3	US-09-382-155-1	Sequence 1, Appli
12	384	73.7	78	3	US-09-074-044A-1	Sequence 1, Appli
13	129.5	24.9	139	3	US-09-382-155-20	Sequence 20, Appl
14	129.5	24.9	139	3	US-09-074-044A-20	Sequence 20, Appl
15	121.5	23.3	241	3	US-09-382-155-21	Sequence 21, Appl
16	121.5	23.3	241	3	US-09-074-044A-21	Sequence 21, Appl
17	119	22.8	371	3	US-09-382-155-22	Sequence 22, Appl
18	119	22.8	371	3	US-09-074-044A-22	Sequence 22, Appl
19	113	21.7	79	3	US-09-382-155-9	Sequence 9, Appli
20	113	21.7	79	3	US-09-074-044A-9	Sequence 9, Appli
21	109	20.9	79	3	US-09-382-155-3	Sequence 3, Appli
22	109	20.9	79	3	US-09-074-044A-3	Sequence 3, Appli
23	102.5	19.7	82	3	US-09-382-155-7	Sequence 7, Appli
24	102.5	19.7	82	3	US-09-074-044A-7	Sequence 7, Appli
25	99.5	19.1	79	3	US-09-074-044A-5	Sequence 5, Appli
26	99.5	19.1	171	3	US-09-382-155-23	Sequence 23, Appl
27	99.5	19.1	171	3	US-09-074-044A-23	Sequence 23, Appl
28	98.5	18.9	180	3	US-09-382-155-18	Sequence 18, Appl
29	98.5	18.9	180	3	US-09-074-044A-18	Sequence 18, Appl
30	98.5	18.9	220	2	US-08-807-200-2	Sequence 2, Appli
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32	98.5	18.9	235	3	US-08-983-502-5	Sequence 5, Appli
33	98.5	18.9	235	4	US-09-516-747-5	Sequence 5, Appli
34	98.5	18.9	235	5	PCT-US96-10521-5	Sequence 5, Appli
35	98.5	18.9	257	1	US-08-618-164-2	Sequence 2, Appli
36	98.5	18.9	261	3	US-08-983-502-25	Sequence 25, Appl
37	98.5	18.9	261	4	US-09-516-747-25	Sequence 25, Appl
38	98.5	18.9	261	5	PCT-US96-10521-25	Sequence 25, Appl
39	98.5	18.9	277	3	US-08-983-502-8	Sequence 8, Appli
40	98.5	18.9	277	4	US-09-516-747-8	Sequence 8, Appli
41	98.5	18.9	277	5	PCT-US96-10521-8	Sequence 6, Appli
42	98.5	18.9	464	3	US-08-983-502-18	Sequence 18, Appl
43	98.5	18.9	464	4	US-09-516-747-18	Sequence 18, Appl
44	98.5	18.9	464	5	PCT-US96-10521-18	Sequence 18, Appl
45	98.5	18.9	478	4	US-09-009-893A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-382-155-17
; Sequence 17, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
; TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382,155B
; CURRENT FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074,044
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-382-155-17

Query Match 96.7%; Score 504; DB 3; Length 221;
Best Local Similarity 99.0%; Pred. No. 2.2e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
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RESULT 2
US-09-074-044A-17
; Sequence 17, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-kB,JNK AND
; TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI

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;       COUNTRY:  USA
;       ZIP:  64108
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/074,044A
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  COLLINS, JOHN M
;       REGISTRATION NUMBER:  26,262
;       REFERENCE/DOCKET NUMBER:  26588
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  816/474-9050
;       TELEFAX:  816/474-9057
;   INFORMATION FOR SEQ ID NO:  17:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  221 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  protein
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
US-09-074-044A-17

  Query Match             96.7%;  Score 504;  DB 3;  Length 221;
  Best Local Similarity   99.0%;  Pred. No. 2.2e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 3
US-08-859-167-2
; Sequence 2, Application US/08859167
; Patent No. 6037461
;  GENERAL INFORMATION:
;    APPLICANT:  Alnemri, Emad S.
;    APPLICANT:  Fernandez-Alnemri, Teresa
;    TITLE OF INVENTION:  FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
;    TITLE OF INVENTION:  USING THE SAME, AND COMPOSITIONS FOR AND METHODS
;    TITLE OF INVENTION:  Of MAKING THE SAME
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461ris
;      STREET:  One Liberty Place, 46th floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  WINDOWS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,167
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  TJU-
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 445 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-859-167-2

  Query Match             96.7%;  Score 504;  DB 3;  Length 445;
  Best Local Similarity   99.0%;  Pred. No. 5.1e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
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Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 4
US-09-109-273-2
; Sequence 2, Application US/09109273
; Patent No. 6063760
;  GENERAL INFORMATION:
;    APPLICANT:  Alnemri, Emad S.
;    APPLICANT:  Fernandez-Alnemri, Teresa
;    TITLE OF INVENTION:  FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
;    TITLE OF INVENTION:  USING THE SAME, AND COMPOSITIONS FOR AND METHODS
;    TITLE OF INVENTION:  Of MAKING THE SAME
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760ris
;      STREET:  One Liberty Place, 46th floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  WINDOWS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/109,273
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/859,167
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  TJU-
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  445 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-109-273-2

  Query Match             96.7%;  Score 504;  DB 3;  Length 445;
  Best Local Similarity   99.0%;  Pred. No. 5.1e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
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Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 5
US-09-276-993-2
; Sequence 2, Application US/09276993
; Patent No. 6207801
;  GENERAL INFORMATION:
;    APPLICANT:  Alnemri, Emad S.
;    APPLICANT:  Fernandez-Alnemri, Teresa
;    TITLE OF INVENTION:  FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
;    TITLE OF INVENTION:  USING THE SAME, AND COMPOSITIONS FOR AND METHODS
;    TITLE OF INVENTION:  Of MAKING THE SAME
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801ris
;      STREET:  One Liberty Place, 46th floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  WINDOWS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/276,993
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/859,167
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  TJU-
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 445 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-276-993-2

  Query Match             96.7%;  Score 504;  DB 3;  Length 445;
  Best Local Similarity   99.0%;  Pred. No. 5.1e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
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Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
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Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 6
US-09-723-450-2
; Sequence 2, Application US/09723450
; Patent No. 6576751
; GENERAL INFORMATION:
;  APPLICANT: Alnemri, Emad S.
;  TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, And
;  TITLE OF INVENTION:  Compositions For And Methods Of Making The Same
;  FILE REFERENCE: TJU2445
;  CURRENT APPLICATION NUMBER: US/09/723,450
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: 09/276,993
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 08/859,167
;  PRIOR FILING DATE: 1997-05-20
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 445
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: No. 6576751el Sequence
US-09-723-450-2

  Query Match             96.7%;  Score 504;  DB 4;  Length 445;
  Best Local Similarity   99.0%;  Pred. No. 5.1e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
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Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
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Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 7
US-08-795-088A-2
; Sequence 2, Application US/08795088A
; Patent No. 6242569
;  GENERAL INFORMATION:
;    APPLICANT:  Sul, Hong-Bing
;    APPLICANT:  Goeddel, David V.
;    TITLE OF INVENTION:  Regulators of Apoptosis
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Science & Technology Law Group
;      STREET:  75 Denise Drive
;      CITY:  Hillsborough
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94010
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,088A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Osman, Richard A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 343-4341
;      TELEFAX:  (650) 343-4342
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  480 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
US-08-795-088A-2
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  Query Match             96.7%;  Score 504;  DB 3;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 5.6e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
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Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 8
US-09-069-023-34
; Sequence 34, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
;  APPLICANT: Nunez, Gabriel
;  APPLICANT: Inohara, Naohiro
;  APPLICANT: Koseki, Takeyoshi
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
;  TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
;  FILE REFERENCE: UM-03333
;  CURRENT APPLICATION NUMBER: US/09/069,023A
;  CURRENT FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
;   LENGTH: 480
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-069-023-34

  Query Match             96.7%;  Score 504;  DB 3;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 5.6e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 9
US-09-009-893A-2
; Sequence 2, Application US/09009893A
; Patent No. 6623938
; GENERAL INFORMATION:
;  APPLICANT:  Ni, Jian
;  APPLICANT:  Rosen, Craig A.
;  APPLICANT:  Dixit, Vishva M.
;  APPLICANT:  Gentz, Reiner L.
;  APPLICANT:  Kenny, Joseph J.
;  TITLE OF INVENTION:   I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Rec
;  TITLE OF INVENTION:  CD-95 Induced Apoptosis
;  FILE REFERENCE:   1488.0970002
;  CURRENT APPLICATION NUMBER: US/09/009,893A
;  CURRENT FILING DATE:  1998-02-21
;  PRIOR APPLICATION NUMBER:   US 60/054,800
;  PRIOR FILING DATE:   1997-08-05
;  PRIOR APPLICATION NUMBER:   US 60/034,205
;  PRIOR FILING DATE:   1997-01-21
;  NUMBER OF SEQ ID NOS:   35
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 480
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-009-893A-2

  Query Match             96.7%;  Score 504;  DB 4;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 5.6e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 10
US-09-489-155-2
; Sequence 2, Application US/09489155
; Patent No. 6680171
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Rosen, Craig A.
;  APPLICANT:  Dixit, Vishva M.
;  APPLICANT:  Gentz, Reiner L.
;  APPLICANT:  Kenny, Joseph J.
;  TITLE OF INVENTION: I-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Recept
;  TITLE OF INVENTION:  CD-95 Induced Apoptosis
;  FILE REFERENCE: 1488.0970002
;  CURRENT APPLICATION NUMBER: US/09/489,155
;  CURRENT FILING DATE:  2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/009,893
;  PRIOR FILING DATE: 1998-01-21
;  PRIOR APPLICATION NUMBER: US 60/034,205
;  PRIOR FILING DATE: 1997-01-21
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 480
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-489-155-2

  Query Match             96.7%;  Score 504;  DB 4;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 5.6e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 11
US-09-382-155-1
; Sequence 1, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
;  APPLICANT: CHAUDHARY, PREET M
;  APPLICANT: HOOD, LEROY
;  TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
;  TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
;  FILE REFERENCE: Chaudhary
;  CURRENT APPLICATION NUMBER: US/09/382,155B
;  CURRENT FILING DATE: 1999-08-24
;  EARLIER APPLICATION NUMBER: 09/074,044
;  EARLIER FILING DATE: 1998-05-07
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 78
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```
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-382-155-1

  Query Match             73.7%;  Score 384;  DB 3;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-38;
  Matches   78;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKA 81
              ||||||||||||||||||
Db         61 RVRRFDLLKRILKMDRKA 78


RESULT 12
US-09-074-044A-1
; Sequence 1, Application US/09074044A
; Patent No. 6207458
;  GENERAL INFORMATION:
;    APPLICANT:  CHAUDHARY, PREET M
;    APPLICANT:  HOOD, LEROY
;    TITLE OF INVENTION:  PROTEINS CAPABLE OF REGULATING NK-kB,JNK AND
;    TITLE OF INVENTION:  APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOVEY, WILLIAMS, TIMMONS & COLLINS
;      STREET:  2405 GRAND BLVD., SUITE 400
;      CITY:  KANSAS CITY
;      STATE:  MISSOURI
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/074,044A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLLINS, JOHN M
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  26588
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  816/474-9050
;      TELEFAX:  816/474-9057
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  78 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-09-074-044A-1

  Query Match             73.7%;  Score 384;  DB 3;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-38;
  Matches   78;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKA 81
              ||||||||||||||||||
Db         61 RVRRFDLLKRILKMDRKA 78


RESULT 13
US-09-382-155-20
; Sequence 20, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
;  APPLICANT: CHAUDHARY, PREET M
;  APPLICANT: HOOD, LEROY
;  TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
;  TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
;  FILE REFERENCE: Chaudhary
;  CURRENT APPLICATION NUMBER: US/09/382,155B
;  CURRENT FILING DATE: 1999-08-24
;  EARLIER APPLICATION NUMBER: 09/074,044
;  EARLIER FILING DATE: 1998-05-07
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 139
;   TYPE: PRT
;   ORGANISM: Molluscum contagiosum virus
US-09-382-155-20

  Query Match             24.9%;  Score 129.5;  DB 3;  Length 139;
  Best Local Similarity   34.0%;  Pred. No. 1.3e-07;
  Matches   35;  Conservative   23;  Mismatches   38;  Indels    7;  Gaps    3;

Qy          7 EVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILR---ERGKLSVGDLAELLY 63
              ||: :|   | ||::|::|||   : : :  | :  |:  ||   | |:|:   ||| |:
Db          5 EVLCEVARKLGTDDREVVLFL---LNVFIPQPTLAQLIGALRALKEEGRLTFPLLAECLF 61

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEI-GE 105
              |  | |||: :| :| : :| ||       | |:: :  : ||
Db         62 RAGRRDLLRDLLHLDPRFLERHLAGTMSYFSPYQLTVLHVDGE 104


RESULT 14
US-09-074-044A-20
; Sequence 20, Application US/09074044A
; Patent No. 6207458
;  GENERAL INFORMATION:
;    APPLICANT:  CHAUDHARY, PREET M
;    APPLICANT:  HOOD, LEROY
;    TITLE OF INVENTION:  PROTEINS CAPABLE OF REGULATING NK-kB,JNK AND
;    TITLE OF INVENTION:  APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOVEY, WILLIAMS, TIMMONS & COLLINS
;      STREET:  2405 GRAND BLVD., SUITE 400
;      CITY:  KANSAS CITY
;      STATE:  MISSOURI
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/074,044A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLLINS, JOHN M
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  26588
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  816/474-9050
;      TELEFAX:  816/474-9057
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  139 amino acids
```

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;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  HUMAN HERPES VIRUS 8
US-09-074-044A-20

  Query Match             24.9%;  Score 129.5;  DB 3;  Length 139;
  Best Local Similarity   34.0%;  Pred. No. 1.3e-07;
  Matches   35;  Conservative   23;  Mismatches   38;  Indels    7;  Gaps    3;

Qy          7 EVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILR---ERGKLSVGDLAELLY 63
              ||: :|   | ||::|::|||   : : :  | :  |:  ||   | |:|:   ||| |:
Db          5 EVLCEVARKLGTDDREVVLFL---LNVFIPQPTLAQLIGALRALKEEGRLTFPLLAECLF 61

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEI-GE 105
              |  | |||: :| :| : :| ||       | |:: :  : ||
Db         62 RAGRRDLLRDLLHLDPRFLERHLAGTMSYFSPYQLTVLHVDGE 104


RESULT 15
US-09-382-155-21
; Sequence 21, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
;  APPLICANT: CHAUDHARY, PREET M
;  APPLICANT: HOOD, LEROY
;  TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
;  TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
;  FILE REFERENCE: Chaudhary
;  CURRENT APPLICATION NUMBER: US/09/382,155B
;  CURRENT FILING DATE: 1999-08-24
;  EARLIER APPLICATION NUMBER: 09/074,044
;  EARLIER FILING DATE: 1998-05-07
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Molluscum contagiosum virus
US-09-382-155-21

  Query Match             23.3%;  Score 121.5;  DB 3;  Length 241;
  Best Local Similarity   36.5%;  Pred. No. 2.2e-06;
  Matches   35;  Conservative   16;  Mismatches   40;  Indels    5;  Gaps    3;

Qy         10 HQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFD 69
              | :|| ||: |  :||||| | |       |   |  | :: ||::  | |:|| ::| |
Db         15 HLLEE-LDSHEDSLLLFLCHDAAPGCT--TVTQALCSLSQQRKLTLAALVEMLYVLQRMD 71

Qy         70 LLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||    : ::  |   |     :: || ||  :||
Db         72 LLKSRFGLSKEGAEQ--LLGTSFLTRYRKLMVCVGE 105


RESULT 16
US-09-074-044A-21
; Sequence 21, Application US/09074044A
; Patent No. 6207458
;  GENERAL INFORMATION:
;    APPLICANT:  CHAUDHARY, PREET M
;    APPLICANT:  HOOD, LEROY
;    TITLE OF INVENTION:  PROTEINS CAPABLE OF REGULATING NK-kB,JNK AND
;    TITLE OF INVENTION:  APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOVEY, WILLIAMS, TIMMONS & COLLINS
;      STREET:  2405 GRAND BLVD., SUITE 400
;      CITY:  KANSAS CITY
;      STATE:  MISSOURI
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/074,044A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLLINS, JOHN M
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  26588
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  816/474-9050
;      TELEFAX:  816/474-9057
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  241 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  MOLLUSCUM CONTAGIOSUM VIRUS
US-09-074-044A-21

  Query Match             23.3%;  Score 121.5;  DB 3;  Length 241;
  Best Local Similarity   36.5%;  Pred. No. 2.2e-06;
  Matches   35;  Conservative   16;  Mismatches   40;  Indels    5;  Gaps    3;

Qy         10 HQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFD 69
              | :|| ||: |  :||||| | |       |   |  | :: ||::  | |:|| ::| |
Db         15 HLLEE-LDSHEDSLLLFLCHDAAPGCT--TVTQALCSLSQQRKLTLAALVEMLYVLQRMD 71

Qy         70 LLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||    : ::  |   |     :: || ||  :||
Db         72 LLKSRFGLSKEGAEQ--LLGTSFLTRYRKLMVCVGE 105


RESULT 17
US-09-382-155-22
; Sequence 22, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
;  APPLICANT: CHAUDHARY, PREET M
;  APPLICANT: HOOD, LEROY
;  TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
;  TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
;  FILE REFERENCE: Chaudhary
;  CURRENT APPLICATION NUMBER: US/09/382,155B
;  CURRENT FILING DATE: 1999-08-24
;  EARLIER APPLICATION NUMBER: 09/074,044
;  EARLIER FILING DATE: 1998-05-07
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 371
;   TYPE: PRT
;   ORGANISM: Molluscum contagiosum virus
US-09-382-155-22

  Query Match             22.8%;  Score 119;  DB 3;  Length 371;
  Best Local Similarity   38.6%;  Pred. No. 7.3e-06;
  Matches   34;  Conservative   12;  Mismatches   38;  Indels    4;  Gaps    2;

Qy         16 LDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRIL 75
              ||  | |:| |||||||         | |  |: |  |::  :||||  :||||:||
Db         18 LDASEHEVLRFLCRDVA--PASKTAEDALRALQRRRLLTLSSMAELLCALRRFDVLKVRF 75

Qy         76 KMDRKAVETHLLRNPHLVSDYRVLMSEI 103
              | |:       |      :| ||: :: |
Db         76 GMTRECAGR--LLGHGFLSQYRLQVAAI 101
```

```
RESULT 18
US-09-074-044A-22
; Sequence 22, Application US/09074044A
; Patent No. 6207458
;  GENERAL INFORMATION:
;    APPLICANT:  CHAUDHARY, PREET M
;    APPLICANT:  HOOD, LEROY
;    TITLE OF INVENTION:  PROTEINS CAPABLE OF REGULATING NK-kB,JNK AND
;    TITLE OF INVENTION:  APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOVEY, WILLIAMS, TIMMONS & COLLINS
;      STREET:  2405 GRAND BLVD., SUITE 400
;      CITY:  KANSAS CITY
;      STATE:  MISSOURI
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/074,044A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLLINS, JOHN M
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  26588
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  816/474-9050
;      TELEFAX:  816/474-9057
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  371 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  MOLLUSCUM CONTAGIOSUM VIRUS
US-09-074-044A-22

  Query Match             22.8%;  Score 119;  DB 3;  Length 371;
  Best Local Similarity   38.6%;  Pred. No. 7.3e-06;
  Matches   34;  Conservative   12;  Mismatches   38;  Indels    4;  Gaps    2;

Qy         16 LDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRIL 75
              ||  | |:| |||||||          | |  |: |  |::  :|||| :||||:||
Db         18 LDASEHEVLRFLCRDVA--PASKTAEDALRALQRRRLLTLSSMAELLCALRRFDVLKVRF 75

Qy         76 KMDRKAVETHLLRNPHLVSDYRVLMSEI 103
              | |:      |     :| ||: :: |
Db         76 GMTRECAGR--LLGHGFLSQYRLQVAAI 101


RESULT 19
US-09-382-155-9
; Sequence 9, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
;  APPLICANT: CHAUDHARY, PREET M
;  APPLICANT: HOOD, LEROY
;  TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
;  TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
;  FILE REFERENCE: Chaudhary
;  CURRENT APPLICATION NUMBER: US/09/382,155B
;  CURRENT FILING DATE: 1999-08-24
;  EARLIER APPLICATION NUMBER: 09/074,044
;  EARLIER FILING DATE: 1998-05-07
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 79
;   TYPE: PRT
;   ORGANISM: Molluscum contagiosum virus
US-09-382-155-9

  Query Match             21.7%;  Score 113;  DB 3;  Length 79;
  Best Local Similarity   45.3%;  Pred. No. 5.5e-06;
  Matches   29;  Conservative    7;  Mismatches   26;  Indels    2;  Gaps    1;

Qy         16 LDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRIL 75
              ||  | |:| |||||||          | |  |: |  |::  :|||| :||||:||
Db         18 LDASEHEVLRFLCRDVA--PASKTAEDALRALQRRRLLTLSSMAELLCALRRFDVLKVRF 75

Qy         76 KMDR 79
              | |
Db         76 GMTR 79


RESULT 20
US-09-074-044A-9
; Sequence 9, Application US/09074044A
; Patent No. 6207458
;  GENERAL INFORMATION:
;    APPLICANT:  CHAUDHARY, PREET M
;    APPLICANT:  HOOD, LEROY
;    TITLE OF INVENTION:  PROTEINS CAPABLE OF REGULATING NK-kB,JNK AND
;    TITLE OF INVENTION:  APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOVEY, WILLIAMS, TIMMONS & COLLINS
;      STREET:  2405 GRAND BLVD., SUITE 400
;      CITY:  KANSAS CITY
;      STATE:  MISSOURI
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/074,044A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLLINS, JOHN M
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  26588
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  816/474-9050
;      TELEFAX:  816/474-9057
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  79 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  MOLLUSCUM CONTAGIOSUM VIRUS
US-09-074-044A-9

  Query Match             21.7%;  Score 113;  DB 3;  Length 79;
  Best Local Similarity   45.3%;  Pred. No. 5.5e-06;
  Matches   29;  Conservative    7;  Mismatches   26;  Indels    2;  Gaps    1;

Qy         16 LDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRIL 75
              ||  | |:| |||||||          | |  |: |  |::  :|||| :||||:||
Db         18 LDASEHEVLRFLCRDVA--PASKTAEDALRALQRRRLLTLSSMAELLCALRRFDVLKVRF 75
```

```
Qy          76 KMDR 79
               | |
Db          76 GMTR 79


RESULT 21
US-09-382-155-3
; Sequence 3, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
;  APPLICANT: CHAUDHARY, PREET M
;  APPLICANT: HOOD, LEROY
;  TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
;  TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
;  FILE REFERENCE: Chaudhary
;  CURRENT APPLICATION NUMBER: US/09/382,155B
;  CURRENT FILING DATE: 1999-08-24
;  EARLIER APPLICATION NUMBER: 09/074,044
;  EARLIER FILING DATE: 1998-05-07
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 79
;   TYPE: PRT
;   ORGANISM: HUMAN HERPESVIRUS 8
US-09-382-155-3

  Query Match             20.9%;  Score 109;  DB 3;  Length 79;
  Best Local Similarity   37.3%;  Pred. No. 1.6e-05;
  Matches   28;  Conservative   17;  Mismatches   24;  Indels    6;  Gaps    2;

Qy           7 EVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILR---ERGKLSVGDLAELLY 63
               ||: :|   | ||::|::|||   : : :  | :  |:  ||   | |:|:   ||| |:
Db           5 EVLCEVARKLGTDDREVVLFL---LNVFIPQPTLAQLIGALRALKEEGRLTFPLLAECLF 61

Qy          64 RVRRFDLLKRILKMD 78
               |  | |||: :| :|
Db          62 RAGRRDLLRDLLHLD 76


RESULT 22
US-09-074-044A-3
; Sequence 3, Application US/09074044A
; Patent No. 6207458
;  GENERAL INFORMATION:
;    APPLICANT:  CHAUDHARY, PREET M
;    APPLICANT:  HOOD, LEROY
;    TITLE OF INVENTION:  PROTEINS CAPABLE OF REGULATING NK-kB,JNK AND
;    TITLE OF INVENTION:  APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOVEY, WILLIAMS, TIMMONS & COLLINS
;      STREET:  2405 GRAND BLVD., SUITE 400
;      CITY:  KANSAS CITY
;      STATE:  MISSOURI
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/074,044A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLLINS, JOHN M
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  26588
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  816/474-9050
;      TELEFAX:  816/474-9057
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  79 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  HUMAN HERPES VIRUS 8
US-09-074-044A-3

  Query Match             20.9%;  Score 109;  DB 3;  Length 79;
  Best Local Similarity   37.3%;  Pred. No. 1.6e-05;
  Matches   28;  Conservative   17;  Mismatches   24;  Indels    6;  Gaps    2;

Qy           7 EVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILR---ERGKLSVGDLAELLY 63
               ||: :|   | ||::|::|||   : : :  | :  |:  ||   | |:|:   ||| |:
Db           5 EVLCEVARKLGTDDREVVLFL---LNVFIPQPTLAQLIGALRALKEEGRLTFPLLAECLF 61

Qy          64 RVRRFDLLKRILKMD 78
               |  | |||: :| :|
Db          62 RAGRRDLLRDLLHLD 76


RESULT 23
US-09-382-155-7
; Sequence 7, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
;  APPLICANT: CHAUDHARY, PREET M
;  APPLICANT: HOOD, LEROY
;  TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
;  TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
;  FILE REFERENCE: Chaudhary
;  CURRENT APPLICATION NUMBER: US/09/382,155B
;  CURRENT FILING DATE: 1999-08-24
;  EARLIER APPLICATION NUMBER: 09/074,044
;  EARLIER FILING DATE: 1998-05-07
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 82
;   TYPE: PRT
;   ORGANISM: Molluscum contagiosum virus
US-09-382-155-7

  Query Match             19.7%;  Score 102.5;  DB 3;  Length 82;
  Best Local Similarity   42.9%;  Pred. No. 9.9e-05;
  Matches   27;  Conservative   10;  Mismatches   23;  Indels    3;  Gaps    2;

Qy          10 HQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFD 69
               | :|| ||: |  :||||| | |       |   |  | :: ||::  | |:|| ::| |
Db          15 HLLEE-LDSHEDSLLLFLCHDAAPGCT--TVTQALCSLSQQRKLTLAALVEMLYVLQRMD 71

Qy          70 LLK 72
               |||
Db          72 LLK 74


RESULT 24
US-09-074-044A-7
; Sequence 7, Application US/09074044A
; Patent No. 6207458
;  GENERAL INFORMATION:
;    APPLICANT:  CHAUDHARY, PREET M
;    APPLICANT:  HOOD, LEROY
;    TITLE OF INVENTION:  PROTEINS CAPABLE OF REGULATING NK-kB,JNK AND
;    TITLE OF INVENTION:  APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOVEY, WILLIAMS, TIMMONS & COLLINS
```

```
;      STREET:  2405 GRAND BLVD., SUITE 400
;      CITY:  KANSAS CITY
;      STATE:  MISSOURI
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/074,044A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLLINS, JOHN M
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  26588
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  816/474-9050
;      TELEFAX:  816/474-9057
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  82 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  MOLLUSCUM CONTAGIOSUM VIRUS
US-09-074-044A-7

  Query Match             19.7%;  Score 102.5;  DB 3;  Length 82;
  Best Local Similarity   42.9%;  Pred. No. 9.9e-05;
  Matches   27;  Conservative   10;  Mismatches   23;  Indels    3;  Gaps    2;

Qy         10 HQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFD 69
              | :|| ||: |  :||||| | |       |   |  | :: ||::  | |:|| ::| |
Db         15 HLLEE-LDSHEDSLLLFLCHDAAPGCT--TVTQALCSLSQQRKLTLAALVEMLYVLQRMD 71

Qy         70 LLK 72
              |||
Db         72 LLK 74


RESULT 25
US-09-074-044A-5
; Sequence 5, Application US/09074044A
; Patent No. 6207458
;  GENERAL INFORMATION:
;    APPLICANT:  CHAUDHARY, PREET M
;    APPLICANT:  HOOD, LEROY
;    TITLE OF INVENTION:  PROTEINS CAPABLE OF REGULATING NK-kB,JNK AND
;    TITLE OF INVENTION:  APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOVEY, WILLIAMS, TIMMONS & COLLINS
;      STREET:  2405 GRAND BLVD., SUITE 400
;      CITY:  KANSAS CITY
;      STATE:  MISSOURI
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/074,044A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLLINS, JOHN M
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  26588
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  816/474-9050
;      TELEFAX:  816/474-9057
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  79 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Equine herpesvirus
US-09-074-044A-5

  Query Match             19.1%;  Score 99.5;  DB 3;  Length 79;
  Best Local Similarity   39.4%;  Pred. No. 0.00021;
  Matches   26;  Conservative    8;  Mismatches   21;  Indels   11;  Gaps    2;

Qy         15 ALDTDEKEMLLFLCRDVAIDVVPPN------VRDLLDILRERGKLSVGDLAELLYRVRRF 68
              :|| || |  |:||||:      |      ||    | :   ||  :  |||:|| |
Db         12 SLDEDETETYLYLCRDLL-----KNKGEFQCTRDAFKFLSDYACLSAANQMELLFRVGRL 66

Qy         69 DLLKRI 74
              ||::||
Db         67 DLIRRI 72


RESULT 26
US-09-382-155-23
; Sequence 23, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
;  APPLICANT: CHAUDHARY, PREET M
;  APPLICANT: HOOD, LEROY
;  TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
;  TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
;  FILE REFERENCE: Chaudhary
;  CURRENT APPLICATION NUMBER: US/09/382,155B
;  CURRENT FILING DATE: 1999-08-24
;  EARLIER APPLICATION NUMBER: 09/074,044
;  EARLIER FILING DATE: 1998-05-07
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;   LENGTH: 171
;   TYPE: PRT
;   ORGANISM: Equine Herpesvirus
US-09-382-155-23

  Query Match             19.1%;  Score 99.5;  DB 3;  Length 171;
  Best Local Similarity   39.4%;  Pred. No. 0.00055;
  Matches   26;  Conservative    8;  Mismatches   21;  Indels   11;  Gaps    2;

Qy         15 ALDTDEKEMLLFLCRDVAIDVVPPN------VRDLLDILRERGKLSVGDLAELLYRVRRF 68
              :|| || |  |:||||:      |      ||    | :   ||  :  |||:|| |
Db         12 SLDEDETETYLYLCRDLL-----KNKGEFQCTRDAFKFLSDYACLSAANQMELLFRVGRL 66

Qy         69 DLLKRI 74
              ||::||
Db         67 DLIRRI 72


RESULT 27
US-09-074-044A-23
; Sequence 23, Application US/09074044A
; Patent No. 6207458
;  GENERAL INFORMATION:
;    APPLICANT:  CHAUDHARY, PREET M
;    APPLICANT:  HOOD, LEROY
```

```
;    TITLE OF INVENTION:  PROTEINS CAPABLE OF REGULATING NK-kB,JNK AND
;    TITLE OF INVENTION:  APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOVEY, WILLIAMS, TIMMONS & COLLINS
;      STREET:  2405 GRAND BLVD., SUITE 400
;      CITY:  KANSAS CITY
;      STATE:  MISSOURI
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/074,044A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLLINS, JOHN M
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  26588
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  816/474-9050
;      TELEFAX:  816/474-9057
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  171 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Equine herpesvirus
US-09-074-044A-23

  Query Match             19.1%;  Score 99.5;  DB 3;  Length 171;
  Best Local Similarity   39.4%;  Pred. No. 0.00055;
  Matches   26;  Conservative    8;  Mismatches   21;  Indels   11;  Gaps    2;

Qy         15 ALDTDEKEMLLFLCRDVAIDVVPPN------VRDLLDILRERGKLSVGDLAELLYRVRRF 68
              :|| || |  |:||||:       |       ||    | :   ||  :  |||:|| |
Db         12 SLDEDETETYLYLCRDLL-----KNKGEFQCTRDAFKFLSDYACLSAANQMELLFRVGRL 66

Qy         69 DLLKRI 74
              ||::||
Db         67 DLIRRI 72


RESULT 28
US-09-382-155-18
; Sequence 18, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
;  APPLICANT: CHAUDHARY, PREET M
;  APPLICANT: HOOD, LEROY
;  TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
;  TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
;  FILE REFERENCE: Chaudhary
;  CURRENT APPLICATION NUMBER: US/09/382,155B
;  CURRENT FILING DATE: 1999-08-24
;  EARLIER APPLICATION NUMBER: 09/074,044
;  EARLIER FILING DATE: 1998-05-07
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-382-155-18

  Query Match             18.9%;  Score 98.5;  DB 3;  Length 180;
  Best Local Similarity   29.4%;  Pred. No. 0.00077;
  Matches   32;  Conservative   26;  Mismatches   34;  Indels   17;  Gaps    6;

Qy          9 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPN----VRDLLDI---LRERGKLSVGDLA-- 59
              :: : | ||:::   | ||    ::| :|      ::| | :   |:|:  |   :|:
Db          7 LYDIGEQLDSEDLASLKFL----SLDYIPQRKQEPIKDALMLFQRLQEKRMLEESNLSFL 62

Qy         60 -ELLYRVRRFDLLKRILKMDRKAVETHLLRNP--HLVSDYRVLMSEIGE 105
               |||:|: | |||   |   :: :|   |: |    :| |||:: :| |
Db         63 KELLFRINRLDLLITYLNTRKEEMERE-LQTPGRAQISAYRVMLYQISE 110


RESULT 29
US-09-074-044A-18
; Sequence 18, Application US/09074044A
; Patent No. 6207458
;  GENERAL INFORMATION:
;    APPLICANT:  CHAUDHARY, PREET M
;    APPLICANT:  HOOD, LEROY
;    TITLE OF INVENTION:  PROTEINS CAPABLE OF REGULATING NK-kB,JNK AND
;    TITLE OF INVENTION:  APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOVEY, WILLIAMS, TIMMONS & COLLINS
;      STREET:  2405 GRAND BLVD., SUITE 400
;      CITY:  KANSAS CITY
;      STATE:  MISSOURI
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/074,044A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLLINS, JOHN M
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  26588
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  816/474-9050
;      TELEFAX:  816/474-9057
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-09-074-044A-18

  Query Match             18.9%;  Score 98.5;  DB 3;  Length 180;
  Best Local Similarity   29.4%;  Pred. No. 0.00077;
  Matches   32;  Conservative   26;  Mismatches   34;  Indels   17;  Gaps    6;

Qy          9 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPN----VRDLLDI---LRERGKLSVGDLA-- 59
              :: : | ||:::   | ||    ::| :|      ::| | :   |:|:  |   :|:
Db          7 LYDIGEQLDSEDLASLKFL----SLDYIPQRKQEPIKDALMLFQRLQEKRMLEESNLSFL 62

Qy         60 -ELLYRVRRFDLLKRILKMDRKAVETHLLRNP--HLVSDYRVLMSEIGE 105
               |||:|: | |||   |   :: :|   |: |    :| |||:: :| |
Db         63 KELLFRINRLDLLITYLNTRKEEMERE-LQTPGRAQISAYRVMLYQISE 110


RESULT 30
US-08-807-200-2
; Sequence 2, Application US/08807200
; Patent No. 5837837
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  Hunter, John J.
;    APPLICANT:  Shigjan, Andrew W.
;    APPLICANT:  Wong, Grace H.W.
;    TITLE OF INVENTION:  NOVEL FORMS OF CASPASE-8 AND
;    TITLE OF INVENTION:  USES THEREFOR
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/807,200
;      FILING DATE:  27-FEB-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meiklejohn, Ph.D., Anita L.
;      REGISTRATION NUMBER:  35,283
;      REFERENCE/DOCKET NUMBER:  07334/021001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  220 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-807-200-2

  Query Match             18.9%;  Score 98.5;  DB 2;  Length 220;
  Best Local Similarity   29.4%;  Pred. No. 0.00098;
  Matches   32;  Conservative   26;  Mismatches   34;  Indels   17;  Gaps    6;

Qy          9 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPN----VRDLLDI---LRERGKLSVGDLA-- 59
              :: : | ||:::   | ||    ::| :|      ::| | :   |:|:  |   :|:
Db          7 LYDIGEQLDSEDLASLKFL----SLDYIPQRKQEPIKDALMLFQRLQEKRMLEESNLSFL 62

Qy         60 -ELLYRVRRFDLLKRILKMDRKAVETHLLRNP--HLVSDYRVLMSEIGE 105
               |||:|: | |||   |   :: :|   |: |    :| |||:: :| |
Db         63 KELLFRINRLDLLITYLNTRKEEMERE-LQTPGRAQISAYRVMLYQISE 110


Search completed: September 30, 2005, 08:02:43
Job time : 43 secs
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OM protein - protein search, using sw model

Run on: September 30, 2005, 07:58:45 ; Search time 71 Seconds
(without alignments)
571.970 Million cell updates/sec

Title: US-09-402-569-2
Perfect score: 521
Sequence: 1 KSRMSAEVIHQVEEALDTDE.....LLRNPHLVSDYRVLMSEIGE 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	516	99.0	104	2	AAW76215	Aaw76215 Human FLI
2	506	97.1	491	3	AAB03964	Aab03964 FLIP with
3	504	96.7	221	2	AAW78904	Aaw78904 Human G1
4	504	96.7	221	2	AAW76630	Aaw76630 Human CFL
5	504	96.7	221	2	AAY05789	Aay05789 Human MAC
6	504	96.7	221	2	AAY57455	Aay57455 Human FLI
7	504	96.7	221	3	AAB03959	Aab03959 FLICE-lik
8	504	96.7	221	4	AAB61117	Aab61117 Human MRI
9	504	96.7	221	4	AAB84802	Aab84802 Huamn MRI
10	504	96.7	221	5	ABB09293	Abb09293 Human FLI
11	504	96.7	227	2	AAY05795	Aay05795 MRIT beta
12	504	96.7	270	5	AAE26110	Aae26110 Human FLA
13	504	96.7	291	3	AAY67420	Aay67420 Usurpin-g
14	504	96.7	445	2	AAW90107	Aaw90107 Human FLA
15	504	96.7	445	5	AAE26086	Aae26086 Human FLA
16	504	96.7	462	3	AAY67419	Aay67419 Usurpin-b
17	504	96.7	462	8	ADR14101	Adr14101 Human NF-
18	504	96.7	480	2	AAW58578	Aaw58578 Human FIN
19	504	96.7	480	2	AAW69715	Aaw69715 Human Cas
20	504	96.7	480	2	AAW69229	Aaw69229 I-FLICE-1
21	504	96.7	480	2	AAW78903	Aaw78903 Human G1
22	504	96.7	480	2	AAW76631	Aaw76631 Human CFL
23	504	96.7	480	2	AAY05787	Aay05787 Human MAC
24	504	96.7	480	2	AAY57454	Aay57454 Human FLI
25	504	96.7	480	3	AAY59414	Aay59414 Human CLA
26	504	96.7	480	3	AAY57606	Aay57606 Human apo
27	504	96.7	480	3	AAY67418	Aay67418 Usurpin-a
28	504	96.7	480	3	AAB03960	Aab03960 FLICE-lik
29	504	96.7	480	5	ABB09294	Abb09294 Human FLI
30	504	96.7	480	7	ADA10615	Ada10615 Human inh
31	504	96.7	480	7	ADJ68469	Adj68469 Human hea
32	504	96.7	480	7	ADN95807	Adn95807 Human BEC
33	504	96.7	480	8	ADJ96510	Adj96510 Human I-F
34	504	96.7	480	8	ADR11312	Adr11312 Human inh
35	504	96.7	480	8	ADP54877	Adp54877 Human PRO
36	488.5	93.8	479	2	AAW76625	Aaw76625 Human FLI
37	465	89.3	93	4	AAM16659	Aam16659 Peptide #
38	465	89.3	93	4	ABB35643	Abb35643 Peptide #
39	465	89.3	93	4	AAM29143	Aam29143 Peptide #
40	465	89.3	93	4	ABB30476	Abb30476 Peptide #
41	465	89.3	93	4	ABB21072	Abb21072 Protein #
42	465	89.3	93	4	AAM68836	Aam68836 Human bon
43	465	89.3	93	4	AAM56459	Aam56459 Human bra
44	465	89.3	93	4	ABG50496	Abg50496 Human liv
45	465	89.3	93	4	AAM04375	Aam04375 Peptide #

ALIGNMENTS

RESULT 1
AAW76215
ID AAW76215 standard; protein; 104 AA.
XX
AC AAW76215;
XX
DT 26-NOV-1998 (first entry)
XX
DE Human FLIP protein.
XX
KW FLIP; FLICE inhibitory protein; human; apoptosis-inhibiting protein;
KW protease; death-inducing signalling complex; apoptosis; diagnosis; AIDS;
KW acquired immune deficiency syndrome; neurodegenerative disease.
XX
OS Homo sapiens.
XX
PN DE19713434-C1.
XX
PD 24-SEP-1998.
XX
PF 01-APR-1997; 97DE-01013434.
XX
PR 01-APR-1997; 97DE-01013434.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Krammer P, Peter M, Scaffidi C;
XX
DR WPI; 1998-482168/42.
DR N-PSDB; AAV46493.
XX
PT Apoptosis-inhibiting FLIP protein and corresponding DNA - useful for
PT inhibiting or diagnosing apoptosis.
XX
PS Claim 1; Fig 1; 5pp; German.
XX
CC This sequence represents a human apoptosis-inhibiting protein, FLIP
CC (FLICE inhibitory protein). FLICE is a protease involved in the death-
CC inducing signalling complex. This protein can be used to inhibit
CC apoptosis and the DNA can be used to diagnose and/or inhibit apoptosis,
CC especially where the apoptosis is associated with AIDS or
CC neurodegenerative diseases
XX
SQ Sequence 104 AA;

Query Match 99.0%; Score 516; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 5.5e-53;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 60

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIG 104
              |||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIG 104
```

RESULT 2
AAB03964
ID AAB03964 standard; protein; 491 AA.
XX
AC AAB03964;
XX
DT 26-FEB-2001 (first entry)
XX
DE FLIP with detectable peptide tag.
XX
KW Chimeric protein; fusion protein; FLICE like inhibitor protein; FLIP;
KW Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;
KW tumour specific antigen; immune response; therapy; prophylaxis;
KW diagnosis; HIV; human immunodeficiency syndrome; AIDS;
KW acquired immune deficiency syndrome; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200059935-A1.
XX
PD 12-OCT-2000.
XX
PF 05-APR-2000; 2000WO-US009002.
XX
PR 05-APR-1999; 99US-0127867P.
PR 06-APR-1999; 99US-0128021P.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PA (PAYA/) PAYA C.
PA (ALGE/) ALGECIRAS-SCHMINICH A.
XX
PI Paya C, Algeciras-Schminich A;
XX
DR WPI; 2000-664988/64.
DR N-PSDB; AAA54301.
XX
PT Fusion polypeptide useful for inhibiting ligand-induced apoptosis,
PT comprises portion of anti-apoptotic polypeptide linked to a transport
PT group.
XX
PS Disclosure; Page 84-85; 89pp; English.
XX
CC A chimeric group or fusion peptide which comprises a portion of an anti-
CC apoptotic polypeptide which inhibits apoptosis of lymphocytes in
CC combination with a transport group is described. The transport group is
CC capable of transporting the chimeric group or fusion peptide across the
CC cell membrane. The anti-apoptotic polypeptide is FLICE-like inhibitor
CC protein (FLIP) which inhibits Fas and TNF mediated apoptosis by
CC inhibiting binding of Caspase-8 to the Fas receptor complex, thus
CC shutting off the downstream Fas signalling pathway. The chimeric group
CC and fusion peptide are useful for inhibiting ligand-induced apoptosis by
CC bringing them into contact with T cells. The chimeric group is useful for
CC expanding T cells in vitro e.g. T cells specific for particular antigens
CC such as tumour-specific antigen, for enhancing immune response and to
CC inhibit the apoptosis of chronically activated T cells e.g. activated
CC CD4^+ T cells in HIV infected patients. The chimeric group is also useful
CC for therapeutic, prophylactic or diagnosis of intracellular delivery of
CC small molecules and macromolecules such as anti-apoptotic polypeptides
CC and nucleic acids encoding such polypeptides
XX
SQ Sequence 491 AA;

```
  Query Match             97.1%;  Score 506;  DB 3;  Length 491;
  Best Local Similarity   97.1%;  Pred. No. 5.7e-51;
  Matches  102;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 60
              |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 KEFMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 68

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||||||:||||
Db         69 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 113
```

RESULT 3
AAW78904
ID AAW78904 standard; protein; 221 AA.
XX
AC AAW78904;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human G1 protein isoform beta (CASH-beta).
XX
KW G1 protein; CASH-beta; human; caspase homologue; Fas receptor; modulator;
KW apoptosis; cell death; inflammation; tumour; HIV; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 2. .73
FT /note= "death domain/MORT module"
FT Domain 93. .142
FT /note= "death domain/MORT module"
XX
PN WO9839435-A1.
XX
PD 11-SEP-1998.
XX
PF 26-FEB-1998; 98WO-IL000098.
XX
PR 03-MAR-1997; 97IL-00120367.
PR 01-MAY-1997; 97IL-00120759.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Wallach D, Goltsev Y, Kovalenko A, Varfolomeev E, Brodianski V;
XX
DR WPI; 1998-495842/42.
DR N-PSDB; AAV52969.
XX
PT New DNA encoding isoforms of G1 protein which bind MORT-1 - and regulate
PT the effects of FAS and tumour necrosis factor receptors, useful for
PT killing of cells e.g. HIV and cancer cells.
XX
PS Claim 13; Fig 2; 132pp; English.
XX
CC This is the amino acid sequence of the beta isoform of novel human G1
CC protein. The sequence is deduced from an isolated skin fibroblast cDNA
CC clone (see AAV52969). G1-beta (also called CASH beta, CASH being caspase
CC homologue) and a longer isoform, G1-alpha (see AAW78903), represent 2
CC splice variants of the G1 protein. These G1 proteins are capable of
CC binding to, or interacting directly or indirectly, via their N-terminal
CC MORT modules, with MORT-1 or with MORT-binding proteins such as Mch4
CC (CASP-10) and MACH (CASP-8), and thereby of binding to the intracellular
CC domain of the FAS-R receptor, to which MORT-1 binds, or of binding to the
CC intracellular domain of the p55 tumour necrosis factor (TNF) receptor, to
CC which TRADD binds and to which TRADD protein MORT-1 binds. Hence, they
CC are considered as mediators or modulators of FAS-R having a role in e.g.
CC the signalling process that is initiated by the binding of FAS ligand to
CC FAS-R, and also having a role in the signalling process initiated by the
CC binding of TNF to p55-R. The longer isoform also has a C-terminal caspase
CC activity region involved in cytotoxic activity. G1 DNA (I) and
CC polypeptide (II), vectors and fragments are used to regulate cell death

```
CC   or inflammatory processes. (II) is used to inhibit cell death, and its
CC   inhibitors augment/enhance the processes. (I) and (II) regulate the FAS-R
CC   ligand or TNF effect on cells carrying an FAS-R or p55-R. Tumour, HIV-
CC   infected or other diseased cells can be treated using a viral vector
CC   encoding a viral surface protein, which binds a specific cell surface
CC   receptor and a sequence encoding (II), which kills the cell. Antisense
CC   oligonucleotides, introduced using the above vector, block the expression
CC   of (II) and can also regulate the above effects. These effects can also
CC   be regulated using a vector encoding a ribozyme that interacts with a
CC   cellular mRNA encoding (II), and allows (II) expression
XX
SQ   Sequence 221 AA;

  Query Match             96.7%;  Score 504;  DB 2;  Length 221;
  Best Local Similarity   99.0%;  Pred. No. 3.7e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 4
AAW76630
ID   AAW76630 standard; protein; 221 AA.
XX
AC   AAW76630;
XX
DT   12-JUL-1999  (first entry)
XX
DE   Human CFLIP-S protein.
XX
KW   Death effector domain; human; murine; anti-apoptotic; treatment;
KW   HIV infection; autoimmune disease; FLIP protein.
XX
OS   Homo sapiens.
XX
PN   DE19713393-A1.
XX
PD   08-OCT-1998.
XX
PF   01-APR-1997;   97DE-01013393.
XX
PR   01-APR-1997;   97DE-01013393.
XX
PA   (TSCH/) TSCHOPP J.
XX
PI   Tschopp J,  Thome M,  Burns K,  Irmler M,  Hahne M,  Schroeter M;
PI   Schneider P,  Bodmer J,  Steiner V,  Rimoldi D,  Hoffmann K,  French EL;
XX
DR   WPI; 1998-532710/46.
DR   N-PSDB; AAV61936.
XX
PT   New DNA encoding for anti-apoptotic gene product - used to treat HIV
PT   infections and autoimmune diseases.
XX
PS   Claim 20; Fig 4A; 45pp; German.
XX
CC   This invention describes novel human and mouse anti-apoptotic gene
CC   products which contain at least one death effector domain. The products
CC   of the invention are used in the treatment of HIV infections and
CC   autoimmune diseases
XX
SQ   Sequence 221 AA;

  Query Match             96.7%;  Score 504;  DB 2;  Length 221;
  Best Local Similarity   99.0%;  Pred. No. 3.7e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 5
AAY05789
ID   AAY05789 standard; protein; 221 AA.
XX
AC   AAY05789;
XX
DT   02-AUG-1999  (first entry)
XX
DE   Human MACH related inducer of toxicity MRIT beta 1.
XX
KW   MRIT beta 1; MACH related inducer of toxicity; human; apoptosis;
KW   pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis;
KW   atherosclerosis; neurodegenerative disease; Alzheimer's disease;
KW   Parkinson's disease; retinitis pigmentosa; stroke; AIDS;
KW   aplastic anaemia; myocardial infarction; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9918230-A2.
XX
PD   15-APR-1999.
XX
PF   07-OCT-1998;   98WO-US021132.
XX
PR   07-OCT-1997;   97US-00946226.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Chaudhary PM;
XX
DR   WPI; 1999-277275/23.
DR   N-PSDB; AAX25510.
XX
PT   Identifying regulators of MACH-related inducer of toxicity.
XX
PS   Example 1; Fig 1H; 78pp; English.
XX
CC   The present sequence represents novel human MACH-related inducer of
CC   toxicity (MRIT) isoform MRIT beta 1, a CED-4 homologue. Multiple isoforms
CC   of MRIT have been identified, some of which function to induce caspase
CC   dependent apoptosis in mammalian cells, e.g. MRIT alpha 1 (see AAY05787)
CC   and MRIT beta 1, while others have anti-apoptotic activity, e.g. MRIT
CC   alpha 2 (see AAY05788). MRIT beta 1 lacks the N-terminal death effector
CC   domain of MRIT alpha 1 but includes a C-terminal caspase ICE homology
CC   domain region. Selective enhancers and inhibitors of MRIT apoptotic
CC   activity can be identified and used to treat diseases mediated by the
CC   dysfunction of programmed cell death or proliferation. A cell
CC   accumulation disorder such as cancer, autoimmune disease, viral
CC   infection, angiogenesis or atherosclerosis is treated by administering an
CC   agent that selectively enhances MRIT apoptotic activity, thereby inducing
CC   apoptosis in a subject. A disorder of cell loss, such as a
CC   neurodegenerative disorder, including Alzheimer's disease, Parkinson's
CC   disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial
CC   infarction or AIDS can be treated by administering an agent that
CC   selectively inhibits MRIT apoptotic activity
XX
SQ   Sequence 221 AA;

  Query Match             96.7%;  Score 504;  DB 2;  Length 221;
  Best Local Similarity   99.0%;  Pred. No. 3.7e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
```

```
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
```

RESULT 6
AAY57455
ID AAY57455 standard; protein; 221 AA.
XX
AC AAY57455;
XX
DT 25-FEB-2000 (first entry)
XX
DE Human FLICE-like inhibitory protein short form protein sequence.
XX
KW Human; FLICE-like inhibitory protein long form; FLIP-L; FLIP-S;
KW FLICE-like inhibitory protein short form; apoptosis inhibitor;
KW arteriosclerosis; vascular wall inflammation; vascular injury;
KW Fas ligand-mediated apoptosis; atherosclerosis; transplant.
XX
OS Homo sapiens.
XX
PN WO9942570-A1.
XX
PD 26-AUG-1999.
XX
PF 19-FEB-1999; 99WO-US003558.
XX
PR 20-FEB-1998; 98US-0075471P.
XX
PA (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
XX
PI Walsh K;
XX
DR WPI; 1999-527469/44.
DR N-PSDB; AAZ39041.
XX
PT Treating conditions characterized by vascular wall inflammation.
XX
PS Example 2; Page 72; 105pp; English.
XX
CC The present sequence represents human FLICE-like inhibitory protein short
CC form, designated FLIP-S. The present invention describes a new treatment
CC of a condition characterised by vascular wall inflammation in a subject
CC comprising administering a FLIP molecule to inhibit Fas ligand-mediated
CC apoptosis of vascular endothelial cells in the subject. The method can be
CC used to treat atherosclerosis, transplant arteriosclerosis and vascular
CC injury
XX
SQ Sequence 221 AA;

```
  Query Match             96.7%;  Score 504;  DB 2;  Length 221;
  Best Local Similarity   99.0%;  Pred. No. 3.7e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
```

RESULT 7
AAB03959
ID AAB03959 standard; protein; 221 AA.
XX
AC AAB03959;
XX
DT 26-FEB-2001 (first entry)
XX
DE FLICE-like inhibitor protein (Genbank Accession No. 2253681).
XX
KW Chimeric protein; fusion protein; FLICE like inhibitor protein; FLIP;
KW Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;
KW tumour specific antigen; immune response; therapy; prophylaxis;
KW diagnosis; HIV; human immunodeficiency syndrome; AIDS;
KW acquired immune deficiency syndrome; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200059935-A1.
XX
PD 12-OCT-2000.
XX
PF 05-APR-2000; 2000WO-US009002.
XX
PR 05-APR-1999; 99US-0127867P.
PR 06-APR-1999; 99US-0128021P.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PA (PAYA/) PAYA C.
PA (ALGE/) ALGECIRAS-SCHMINICH A.
XX
PI Paya C, Algeciras-Schminich A;
XX
DR WPI; 2000-664988/64.
XX
PT Fusion polypeptide useful for inhibiting ligand-induced apoptosis,
PT comprises portion of anti-apoptotic polypeptide linked to a transport
PT group.
XX
PS Disclosure; Page 78-79; 89pp; English.
XX
CC A chimeric group or fusion peptide which comprises a portion of an anti-
CC apoptotic polypeptide which inhibits apoptosis of lymphocytes in
CC combination with a transport group is described. The transport group is
CC capable of transporting the chimeric group or fusion peptide across the
CC cell membrane. The anti-apoptotic polypeptide is FLICE-like inhibitor
CC protein (FLIP) which inhibits Fas and TNF mediated apoptosis by
CC inhibiting binding of Caspase-8 to the Fas receptor complex, thus
CC shutting off the downstream Fas signalling pathway. The chimeric group
CC and fusion peptide are useful for inhibiting ligand-induced apoptosis by
CC bringing them into contact with T cells. The chimeric group is useful for
CC expanding T cells in vitro e.g. T cells specific for particular antigens
CC such as tumour-specific antigen, for enhancing immune response and to
CC inhibit the apoptosis of chronically activated T cells e.g. activated
CC CD4^+ T cells in HIV infected patients. The chimeric group is also useful
CC for therapeutic, prophylactic or diagnosis of intracellular delivery of
CC small molecules and macromolecules such as anti-apoptotic polypeptides
CC and nucleic acids encoding such polypeptides
XX
SQ Sequence 221 AA;

```
  Query Match             96.7%;  Score 504;  DB 3;  Length 221;
  Best Local Similarity   99.0%;  Pred. No. 3.7e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
```

RESULT 8
AAB61117
ID AAB61117 standard; protein; 221 AA.
XX
AC AAB61117;

XX
DT 02-MAY-2001 (first entry)
XX
DE Human MRITalpha.
XX
KW Human; MRITalpha; apoptotic; nuclear factor-kappa B; NF-kB;
KW Jun N-terminal kinase; JuNK; apoptosis; Caspase-8 mutant.
XX
OS Homo sapiens.
XX
PN US6160095-A.
XX
PD 12-DEC-2000.
XX
PF 24-AUG-1999; 99US-00382155.
XX
PR 07-MAY-1998; 98US-00074044.
XX
PA (UNIW) UNIV WASHINGTON.
PA (STOW-) STOWERS INST MEDICAL RES.
XX
PI Hood L, Chaudhary PM;
XX
DR WPI; 2001-101569/11.
XX
PT Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
PT nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
PT for therapeutic purposes.
XX
PS Example 8; Col 43-46; 60pp; English.
XX
CC The present sequence has been shown to regulate the nuclear factor-kappa
CC B (NF-kB), Jun N-terminal kinase (JuNK) and apoptosis pathways. It is
CC provided in a specification relating to novel mutants (D73A, L74A and
CC L75A) for Caspase-8, which are also useful for regulating NF-kB, JuNK and
CC apoptosis activities. The Caspase-8 mutants are useful for therapeutic
CC purposes and in test methods or assays for determining whether a
CC candidate compound has a significant effect upon cell activities,
CC especially NF-kB, JuNK and apoptosis, so as to facilitate the discovery
CC and/or design of therapeutic agents
XX
SQ Sequence 221 AA;

Query Match 96.7%; Score 504; DB 4; Length 221;
Best Local Similarity 99.0%; Pred. No. 3.7e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy 64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
|||||||||||||||||||||||||||||||||||:||||
Db 61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 9
AAB84802
ID AAB84802 standard; protein; 221 AA.
XX
AC AAB84802;
XX
DT 12-JUL-2001 (first entry)
XX
DE Huamn MRIT prodomain.
XX
KW NF-kappaB; JNK; apoptosis; death effector domain; DED.
XX
OS Homo sapiens.
XX
PN US6207458-B1.
XX
PD 27-MAR-2001.
XX
PF 07-MAY-1998; 98US-00074044.
XX
PR 07-MAY-1998; 98US-00074044.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Chaudhary PM, Hood L;
XX
DR WPI; 2001-342087/36.
XX
PT Testing candidate compound affecting cellular NFkappaB JNK, apoptosis
PT activity by comparing cell activity in presence and absence of
PT proteinaceous species having two death effector domain and test compound.
XX
PS Disclosure; Col 47-50; 62pp; English.
XX
CC The present invention relates to testing candidate compounds to determine
CC whether they affect NF-kappaB, JNK and apoptosis activity. The method
CC involves the use of 2 death effector domains (DED). The The compounds
CC identified by the invention have therapeutic applications and are useful
CC for regulating cellular NFkappaB, JNK and apoptosis activity. The assay
CC is useful for identifying pharmacological agents or lead compounds
CC generally involved in assaying for compounds which regulate or modulate a
CC cell activity. The present sequence is a prodoamin used in the invention
XX
SQ Sequence 221 AA;

Query Match 96.7%; Score 504; DB 4; Length 221;
Best Local Similarity 99.0%; Pred. No. 3.7e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy 64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
|||||||||||||||||||||||||||||||||||:||||
Db 61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 10
ABB09293
ID ABB09293 standard; protein; 221 AA.
XX
AC ABB09293;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human FLIP-c protein SEQ ID NO:10.
XX
KW Human; FLIP-c; caspase 8 dominant negative regulator; antiinflammatory;
KW anti-tumour; FLIP-c inhibitor; apoptosis; antisense gene therapy;
KW phosphorothioate; antisense modulation; infection; inflammation; tumour.
XX
OS Homo sapiens.
XX
PN WO200224717-A1.
XX
PD 28-MAR-2002.
XX
PF 14-SEP-2001; 2001WO-US028732.
XX
PR 20-SEP-2000; 2000US-00666269.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ackermann EJ, Bennett CF, Zhang H, Watt AT, Ricketts W, Dean NM;
XX
DR WPI; 2002-404948/43.
DR N-PSDB; ABL52332.
XX
PT Novel antisense compound that hybridizes and inhibits nucleic acid

```
PT   encoding a natural dominant negative regulator of caspase 8, FLIP-c,
PT   useful for preventing or delaying infection, inflammation or tumor
PT   formation.
XX
PS   Example 13; Page 116-117; 154pp; English.
XX
CC   The present invention describes a compound (I) 8-50 nucleobases in length
CC   targeted to a nucleic acid molecule (II) encoding a natural dominant
CC   negative regulator of caspase 8, FLIP-c, where (I) specifically
CC   hybridises with and inhibits expression of the protein, or specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on
CC   (II). (I) has antiinflammatory and anti-tumour activities. (I) is an
CC   inhibitor of FLIP-c expression, a modulator of apoptosis and can be used
CC   in antisense gene therapy. (I) is useful for inhibiting the expression of
CC   FLIP-c in cells or tissues, and for treating an animal having a disease
CC   or condition associated with FLIP-c. (I) is also useful for modulating
CC   apoptosis in a cell, where a caspase such as caspase 8, caspase 3 or
CC   caspase 7 is activated, and the FLIP-c is the long form of FLIP-c. (I) is
CC   also useful for diagnostics, therapeutics, prophylaxis, as research
CC   reagents and kits, for distinguishing functions of various members of a
CC   biological pathway, and in antisense gene therapy. (I) is also useful
CC   prophylactically, e.g., to prevent or delay infection, inflammation or
CC   tumour formation. The present sequence represents human FLIP-c as given
CC   in an example from the present invention
XX
SQ   Sequence 221 AA;

  Query Match             96.7%;  Score 504;  DB 5;  Length 221;
  Best Local Similarity   99.0%;  Pred. No. 3.7e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 11
AAY05795
ID   AAY05795 standard; protein; 227 AA.
XX
AC   AAY05795;
XX
DT   02-AUG-1999  (first entry)
XX
DE   MRIT beta 2 polypeptide.
XX
KW   MRIT beta 2; MACH related inducer of toxicity; human; apoptosis;
KW   anti-apoptotic; cancer; autoimmune disease; angiogenesis;
KW   atherosclerosis; neurodegenerative disease; Alzheimer's disease;
KW   Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
KW   aplastic anaemia; myocardial infarction; therapy; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9918230-A2.
XX
PD   15-APR-1999.
XX
PF   07-OCT-1998;   98WO-US021132.
XX
PR   07-OCT-1997;   97US-00946226.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Chaudhary PM;
XX
DR   WPI; 1999-277275/23.
XX
PT   Identifying regulators of MACH-related inducer of toxicity.
XX
PS   Example 2; Page; 78pp; English.
XX
CC   The present sequence represents MRIT beta 2, comprising amino acid
CC   residues 1-227 of novel human MACH-related inducer of toxicity MRIT alpha
CC   1 (see AAY05787). This deletion mutant was used to examine the
CC   interaction of MRIT alpha 1 with caspases. The results indicated that the
CC   C-terminal 216 residues of MRIT are not sufficient for FLICE-p20
CC   interaction. The invention provides multiple isoforms of MRIT (see
CC   AAY05787-89), isolated active fragments of which have either pro-
CC   apoptotic or anti-apoptotic activity. Selective enhancers and inhibitors
CC   of MRIT apoptotic activity can be identified and used to treat diseases
CC   mediated by the dysfunction of programmed cell death or proliferation,
CC   such as cancer or a neurodegenerative disorder. Note: the present
CC   sequence is not shown in the specification but is derived from the MRIT
CC   alpha 1 sequence given in figure 1F
XX
SQ   Sequence 227 AA;

  Query Match             96.7%;  Score 504;  DB 2;  Length 227;
  Best Local Similarity   99.0%;  Pred. No. 3.8e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 12
AAE26110
ID   AAE26110 standard; protein; 270 AA.
XX
AC   AAE26110;
XX
DT   14-NOV-2002  (first entry)
XX
DE   Human FLAME-1b protein.
XX
KW   Human; FADD-like apoptotic/anti-apoptotic protein; Alzheimer's disease;
KW   gene therapy; human immunodeficiency virus; HIV infection; apoptosis;
KW   FLAME-1b.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          232. .270
FT                   /note= "FLAME-1b unique region"
XX
PN   US2002086983-A1.
XX
PD   04-JUL-2002.
XX
PF   22-AUG-2001; 2001US-00935223.
XX
PR   28-OCT-1997;   97US-00959167.
PR   26-MAR-1999;   99US-00276993.
PR   28-NOV-2000; 2000US-00723450.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Alnemri ES;
XX
DR   WPI; 2002-642259/69.
XX
PT   Novel FADD-like apoptotic/anti-apoptotic proteins useful for inhibiting
PT   apoptosis, treating diseases characterized by apoptosis e.g. HIV
PT   infection and Alzheimer's disease, and for identifying modulators of the
PT   protein.
```

XX
PS Example; Fig 1A; 35pp; English.
XX
CC The invention relates to FADD-like apoptotic/anti-apoptotic proteins
CC (FLAME 1 or 2) and nucleic acid molecules encoding such proteins. FLAME
CC sequences are useful for inhibiting apoptosis and for gene therapy of
CC diseases characterised by apoptosis including HIV infection and
CC Alzheimer's disease. FLAME inhibitors are useful as apoptotic agents and
CC activators are useful as anti-apoptotic agents. FLAME-1 is useful as a
CC substrate for caspase in assays to identify caspase inhibitors. The
CC present sequence is human FLAME-1b protein
XX
SQ Sequence 270 AA;

Query Match 96.7%; Score 504; DB 5; Length 270;
Best Local Similarity 99.0%; Pred. No. 4.7e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy 64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
|||||||||||||||||||||||||||||||||||:||||
Db 61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 13
AAY67420
ID AAY67420 standard; protein; 291 AA.
XX
AC AAY67420;
XX
DT 12-MAY-2000 (first entry)
XX
DE Usurpin-gamma polypeptide.
XX
KW Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta;
KW usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
KW caspase; cytostatic; antiParkinsonian; antidiabetic.
XX
OS Homo sapiens.
XX
PN WO200003023-A1.
XX
PD 20-JAN-2000.
XX
PF 07-JUL-1999; 99WO-CA000615.
XX
PR 08-JUL-1998; 98US-0092005P.
XX
PA (MERI) MERCK FROSST CANADA INC.
XX
PI Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;
XX
DR WPI; 2000-160929/14.
DR N-PSDB; AAZ56989.
XX
PT Novel recombinant DNA molecules and polypeptides for treating apoptosis
PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
PT disease.
XX
PS Claim 6; Fig 11B; 69pp; English.
XX
CC The invention provides recombinant nucleic acid molecules encoding
CC usurpin-alpha (lacking the first death effector domain (DED) or its
CC prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are
CC useful for in vitro and in vivo identification of usurpin-procaspase-8
CC interaction inhibitor. Usurpin is useful as modulator of the sensitivity
CC of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
CC is useful for treating diseases like autoimmune diabetes, cancer and
CC Parkinson's disease. Activators and inhibitors of usurpin-procaspase-8
CC interaction are also useful for treating various diseases mediated by
CC apoptosis. Usurpin provides an attractive model for modulating caspase
CC activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be
CC regulated at several levels in the presence of usurpin, conferring
CC resistance to Fas-ligand cell death. The present sequence represents the
CC usurpin-gamma polypeptide
XX
SQ Sequence 291 AA;

Query Match 96.7%; Score 504; DB 3; Length 291;
Best Local Similarity 99.0%; Pred. No. 5.2e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy 64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
|||||||||||||||||||||||||||||||||||:||||
Db 61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 14
AAW90107
ID AAW90107 standard; protein; 445 AA.
XX
AC AAW90107;
XX
DT 12-APR-1999 (first entry)
XX
DE Human FLAME-1 protein.
XX
KW FLAME-1; FADD-like apoptotic/anti-apoptotic molecule; human; apoptosis;
KW HIV; infection; Alzheimer's disease; cancer; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1. .341
FT /note= "p39 subunit, specifically claimed in Claim 3"
FT Region 5. .71
FT /note= "FADD-DED homology A"
FT Region 90. .168
FT /note= "FADD-DED homology B"
FT Region 197. .445
FT /note= "caspase-domain homology region"
FT Active-site 322. .327
FT /note= "active site motif"
FT Cleavage-site 338. .342
FT /note= "caspase cleavage site, generating p39 and p12"
FT Domain 342. .445
FT /note= "p12 subunit, specifically claimed in Claim 4"
XX
PN WO9852963-A1.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US010200.
XX
PR 20-MAY-1997; 97US-00859167.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Alnemri ES;
XX
DR WPI; 1999-045296/04.
DR N-PSDB; AAV74136.
XX
PT New isolated FADD-like anti-apoptotic molecules - used to develop
PT apoptotic and anti-apoptotic agents for treating, e.g. HIV infection,
PT Alzheimer's disease or neoplastic conditions.
XX
PS Claim 2; Page 39-40; 68pp; English.
XX

CC This is the amino acid sequence of human FLAME-1, or FADD-like
CC apoptotic/anti-apoptotic molecule 1. FLAME-1 is a novel anti-apoptotic
CC protein that interacts specifically with FADD, Mch4, Mch5 and FLAME-2. It
CC is recruited to the Fas receptor complex and can abrogate Fas/TNF-induced
CC apoptosis upon expression in Fas/TNF-sensitive MCF-7 cells. Despite
CC having a caspase domain-like region, it does not have caspase activity.
CC The amino acid sequence of FLAME-1 was deduced from the nucleotide
CC sequence (see AAV74136) of a Jurkat cell-derived cDNA clone. Host cells,
CC recombinant vectors, and methods of using FLAME-1 to identify substrates,
CC activators or inhibitors of FLAME-1 are provided. FLAME-1, FLAME-2 (see
CC AAW90108) and agonists can be used to inhibit apoptosis, e.g. for
CC treating HIV infection or Alzheimer's disease. Inhibitors can be used as
CC apoptotic agents
XX
SQ Sequence 445 AA;

```
  Query Match             96.7%;  Score 504;  DB 2;  Length 445;
  Best Local Similarity   99.0%;  Pred. No. 8.8e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
```

RESULT 15
AAE26086
ID AAE26086 standard; protein; 445 AA.
XX
AC AAE26086;
XX
DT 14-NOV-2002 (first entry)
XX
DE Human FLAME-1 protein.
XX
KW Human; FADD-like apoptotic/anti-apoptotic protein; Alzheimer's disease;
KW gene therapy; human immunodeficiency virus; HIV infection; apoptosis;
KW FLAME-1.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 5. .71
FT /note= "FADD-DED-Homology A (FDH-A) region"
FT Region 90. .168
FT /note= "FADD-DED-Homology B (FDH-B) region"
FT Region 197. .445
FT /note= "Caspase-domain homology (CDH) region"
FT Active-site 323. .327
FT Cleavage-site 338. .342
FT /note= "Caspase cleavage site"
XX
PN US2002086983-A1.
XX
PD 04-JUL-2002.
XX
PF 22-AUG-2001; 2001US-00935223.
XX
PR 28-OCT-1997; 97US-00959167.
PR 26-MAR-1999; 99US-00276993.
PR 28-NOV-2000; 2000US-00723450.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Alnemri ES;
XX
DR WPI; 2002-642259/69.
DR N-PSDB; AAD43202.
XX
PT Novel FADD-like apoptotic/anti-apoptotic proteins useful for inhibiting
PT apoptosis, treating diseases characterized by apoptosis e.g. HIV
PT infection and Alzheimer's disease, and for identifying modulators of the
PT protein.
XX
PS Claim 1; Page 14-15; 35pp; English.
XX
CC The invention relates to FADD-like apoptotic/anti-apoptotic proteins
CC (FLAME 1 or 2) and nucleic acid molecules encoding such proteins. FLAME
CC sequences are useful for inhibiting apoptosis and for gene therapy of
CC diseases characterised by apoptosis including HIV infection and
CC Alzheimer's disease. FLAME inhibitors are useful as apoptotic agents and
CC activators are useful as anti-apoptotic agents. FLAME-1 is useful as a
CC substrate for caspase in assays to identify caspase inhibitors. The
CC present sequence is human FLAME-1 protein
XX
SQ Sequence 445 AA;

```
  Query Match             96.7%;  Score 504;  DB 5;  Length 445;
  Best Local Similarity   99.0%;  Pred. No. 8.8e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
```

RESULT 16
AAY67419
ID AAY67419 standard; protein; 462 AA.
XX
AC AAY67419;
XX
DT 12-MAY-2000 (first entry)
XX
DE Usurpin-beta polypeptide.
XX
KW Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta;
KW usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
KW caspase; cytostatic; antiParkinsonian; antidiabetic.
XX
OS Homo sapiens.
XX
PN WO200003023-A1.
XX
PD 20-JAN-2000.
XX
PF 07-JUL-1999; 99WO-CA000615.
XX
PR 08-JUL-1998; 98US-0092005P.
XX
PA (MERI) MERCK FROSST CANADA INC.
XX
PI Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;
XX
DR WPI; 2000-160929/14.
DR N-PSDB; AAZ56988.
XX
PT Novel recombinant DNA molecules and polypeptides for treating apoptosis
PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
PT disease.
XX
PS Claim 6; Fig 10B; 69pp; English.
XX
CC The invention provides recombinant nucleic acid molecules encoding
CC usurpin-alpha (lacking the first death effector domain (DED) or its
CC prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are
CC useful for in vitro and in vivo identification of usurpin-procaspase-8
CC interaction inhibitor. Usurpin is useful as modulator of the sensitivity

```
CC   of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
CC   is useful for treating diseases like autoimmune diabetes, cancer and
CC   Parkinson's disease. Activators and inhibitors of usurpin-procaspase-8
CC   interaction are also useful for treating various diseases mediated by
CC   apoptosis. Usurpin provides an attractive model for modulating caspase
CC   activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be
CC   regulated at several levels in the presence of usurpin, conferring
CC   resistance to Fas-ligand cell death. The present sequence represents the
CC   usurpin-beta polypeptide
XX
SQ   Sequence 462 AA;

  Query Match             96.7%;  Score 504;  DB 3;  Length 462;
  Best Local Similarity   99.0%;  Pred. No. 9.2e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 17
ADR14101
ID   ADR14101 standard; protein; 462 AA.
XX
AC   ADR14101;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Human NF-kappaB pathway-associated protein SeqID102.
XX
KW   NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
KW   antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
KW   antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
KW   immunosuppressive; vulnerary; gene therapy; immune disorder;
KW   inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
KW   hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW   hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
KW   X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW   viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
KW   viral replication; host cell survival; evasion of immune response;
KW   rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
KW   atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW   autoimmune disorder; hyper immune activity;
KW   aberrant acute phase response; hypercongenital condition; birth defect;
KW   necrotic lesion; wound; organ transplant rejection;
KW   aberrant signal transduction; proliferating disorder; cancer;
KW   HIV propagation; human.
XX
OS   Homo sapiens.
XX
PN   WO2004065577-A2.
XX
PD   05-AUG-2004.
XX
PF   13-JAN-2004; 2004WO-US000798.
XX
PR   14-JAN-2003; 2003US-0440068P.
PR   12-MAY-2003; 2003US-0469757P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Nadler SG,  Neubauer MG,  Feder JN,  Carman J;
XX
DR   WPI; 2004-562168/54.
DR   N-PSDB; ADR14100.
XX
PT   New isolated polynucleotides and polypeptides associated with NF-kappaB
PT   pathway, useful for diagnosing, treating, or preventing disorders or
PT   diseases associated with NF-kappaB pathway.
XX
PS   Claim 6; SEQ ID NO 102; 237pp; English.
XX
CC   This invention relates to the novel association of protein sequences (and
CC   the genes which encode them) to the NF-kappaB pathway. The invention may
CC   be useful for the production of compounds with an antiinflammatory,
CC   cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
CC   gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,
CC   immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
CC   vulnerary activity or for gene therapy. The proteins and nucleotides are
CC   useful for diagnosing, preventing, treating, or ameliorating conditions
CC   or diseases associated with the NF-kappaB pathway. The condition is an
CC   immune disorder, an inflammatory disorder, an inflammatory disorder
CC   related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
CC   hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
CC   syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
CC   ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
CC   hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
CC   survival, evasion of immune responses, rheumatoid arthritis, inflammatory
CC   bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
CC   syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
CC   immune activity, disorders related to aberrant acute phase responses,
CC   hypercongenital conditions, birth defects, necrotic lesions, wounds,
CC   organ transplant rejection, conditions related to organ transplant
CC   rejection, disorders related to aberrant signal transduction,
CC   proliferating disorders, cancers and HIV propagation in cells infected
CC   with other viruses. The present sequence is that of a human protein which
CC   is subject to the novel association with the NF-kappaB pathway of the
CC   invention. Note: This sequence does not appear in the specification but
CC   was obtained by the indexer from Genbank.
XX
SQ   Sequence 462 AA;

  Query Match             96.7%;  Score 504;  DB 8;  Length 462;
  Best Local Similarity   99.0%;  Pred. No. 9.2e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 18
AAW58578
ID   AAW58578 standard; protein; 480 AA.
XX
AC   AAW58578;
XX
DT   07-SEP-1998  (first entry)
XX
DE   Human FIN-1.
XX
KW   Human; FIN-1; FLICE inhibitor-1; ICE-LAP7; death effector domain; DED;
KW   apoptosis-related protein; caspase; viral infection; cancer; tumour;
KW   diagnosis; ischaemic injury; neuro-degenerative disorder.
XX
OS   Homo sapiens.
XX
PN   EP841399-A2.
XX
PD   13-MAY-1998.
XX
PF   10-NOV-1997;   97EP-00309003.
XX
PR   12-NOV-1996;   96US-00748086.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
```

PI Kikly K, Emery JG;
XX
DR WPI; 1998-252943/23.
DR N-PSDB; AAV31375.
XX
PT New nucleic acid encoding human apoptosis-related protein - used for
PT diagnosis and treatment of e.g. viral infections, tumour, ischaemic
PT injury and neuro-degenerative disorders.
XX
PS Claim 11; Page 25-27; 48pp; English.
XX
CC The present sequence represents human FIN-1 (FLICE inhibitor-1), which is
CC a caspase. FLICE (ICE-LAP7) is a protease of the interleukin-converting
CC enzyme family, a protein involved in the regulation of cell death. A host
CC cell, comprising a vector containing FIN-1 encoding DNA, can be used to
CC produce FIN-1. The vector containing the DNA can be used for producing a
CC cell which expresses a polypeptide by transforming or transfecting the
CC cell with it so that the cell expresses the polypeptide encoded the human
CC cDNA contained in the vector. The polypeptide or its antagonist can be
CC used in the treatment of patients needing FIN-1 by in-vivo
CC administration. Conditions which may be treated include viral infection,
CC tumours (especially solid tumours), ischaemic injury (e.g. stroke or
CC myocardial infarction), neurodegenerative disorders (e.g. Alzheimer's or
CC Parkinson's disease), osteoporosis, osteoarthritis, polycystic kidney
CC disease, chronic degenerative liver disease, acquired immunodeficiency
CC syndrome (AIDS) and aplastic anaemia. The polynucleotides may also be
CC used for chromosome identification
XX
SQ Sequence 480 AA;

Query Match 96.7%; Score 504; DB 2; Length 480;
Best Local Similarity 99.0%; Pred. No. 9.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy 64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
|||||||||||||||||||||||||||||||||||||:||||
Db 61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 19
AAW69715
ID AAW69715 standard; protein; 480 AA.
XX
AC AAW69715;
XX
DT 24-NOV-1998 (first entry)
XX
DE Human Casper protein.
XX
KW Casper; caspase-eight-related protein; human; apoptosis.
XX
OS Homo sapiens.
XX
PN WO9833883-A1.
XX
PD 06-AUG-1998.
XX
PF 05-FEB-1998; 98WO-US002117.
XX
PR 05-FEB-1997; 97US-00795088.
XX
PA (TULA-) TULARIK INC.
XX
PI Shu H, Goeddel DV;
XX
DR WPI; 1998-437440/37.
DR N-PSDB; AAV50436.
XX
PT New Casper protein involved in regulation of apoptosis - used, e.g. to
PT identify specific modulators, identify or isolate similar sequences and
PT in gene therapy.
XX
PS Claim 1; Page 22-23; 29pp; English.
XX
CC This is the amino acid sequence of a novel human protein, designated
CC Casper (for caspase-eight-related protein), that is involved in
CC regulation of apoptosis. The sequence is deduced from an isolated cDNA
CC clone (see AAV50436). Casper protein interacts with FADD and is recruited
CC to Fas. It also interacts with caspase-8 and caspase-3, and with TRAF1
CC and TRAF2. A claimed isolated polypeptide comprises the full-length
CC Casper amino acid sequence, or a fragment of at least 6 consecutive amino
CC acid residues including at least one of residues 1-96, 1-202, 1-435, 78-
CC 480, 192-480, 390-480 or residue 360. The isolated protein, or cells that
CC express the protein, can be used to screen for agents, e.g. antibodies or
CC T-cell receptors, that specifically modify the binding of Casper to a
CC target, and thus its function
XX
SQ Sequence 480 AA;

Query Match 96.7%; Score 504; DB 2; Length 480;
Best Local Similarity 99.0%; Pred. No. 9.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy 64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
|||||||||||||||||||||||||||||||||||||:||||
Db 61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 20
AAW69229
ID AAW69229 standard; protein; 480 AA.
XX
AC AAW69229;
XX
DT 16-OCT-1998 (first entry)
XX
DE I-FLICE-1 protein.
XX
KW I-FLICE-1; FADD like ICE protein; inhibitor; TNFR-1; Alzheimer's disease;
KW CD-95 induced apoptosis; Parkinson's disease; rheumatoid arthritis;
KW CNS inflammation; osteoporosis; ischaemia; polycystic kidney disease;
KW multiple sclerosis; head injury; cancer; autoimmune disorder; therapy;
KW viral infection; graft versus host disease; graft rejection.
XX
OS Homo sapiens.
XX
PN WO9831801-A1.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US000969.
XX
PR 21-JAN-1997; 97US-0034205P.
PR 05-AUG-1997; 97US-0054800P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
XX
PI Ni J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;
XX
DR WPI; 1998-414100/35.
DR N-PSDB; AAV44806.
XX
PT New inhibitory polypeptides of FLICE - used to develop products for
PT treating e.g. Alzheimer's disease, sepsis, stroke, osteoporosis, cancers,
PT autoimmune disorders, viral infection or graft rejection.
XX
PS Claim 9; Fig 1; 118pp; English.

```
XX
CC   This sequence is an inhibitor of of Fas-ligand associated with death
CC   domain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-1. The
CC   proteins can inhibit both TNFR-1 and CD-95 induced apoptosis. These are
CC   the first examples of a naturally occurring catalytically inactive
CC   caspase that can act as a dominant negative inhibitor of apoptosis. The
CC   polypeptides and agonists can be used for treating e.g. Alzheimer's
CC   disease, Parkinson's disease, rheumatoid arthritis, septic shock, sepsis,
CC   stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury,
CC   cell death associated with cardiovascular disease, polycystic kidney
CC   disease, apoptosis of endothelial cells in cardiovascular disease,
CC   degenerative liver disease, multiple sclerosis (MS) and head injury
CC   damage. Antagonists of the polypeptides can be used for treating cancers
CC   (e.g. follicular lymphomas, carcinomas with p53 mutations, hormone-
CC   dependent tumours, and cancers of the breast, ovary, prostate, bone,
CC   liver, lung, pancreas, and spleen), autoimmune disorders (e.g. systemic
CC   lupus erythematosus, immune-related glomerulonephritis, rheumatoid
CC   arthritis), and viral infections (e.g. herpes viruses, pox viruses and
CC   adenoviruses), graft versus host disease, acute disease, acute graft
CC   rejection, and chronic graft rejection. The products can also be used for
CC   detection, diagnosis and drug screening
XX
SQ   Sequence 480 AA;

  Query Match             96.7%;  Score 504;  DB 2;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 9.6e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 21
AAW78903
ID   AAW78903 standard; protein; 480 AA.
XX
AC   AAW78903;
XX
DT   11-JAN-1999  (first entry)
XX
DE   Human G1 protein isoform alpha (CASH-alpha).
XX
KW   G1 protein; CASH-alpha; human; caspase homologue; Fas receptor;
KW   modulator; apoptosis; cell death; inflammation; tumour; HIV; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          2. .73
FT                   /note= "death domain/MORT module"
FT   Domain          93. .142
FT                   /note= "death domain/MORT module"
XX
PN   WO9839435-A1.
XX
PD   11-SEP-1998.
XX
PF   26-FEB-1998;   98WO-IL000098.
XX
PR   03-MAR-1997;   97IL-00120367.
PR   01-MAY-1997;   97IL-00120759.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Wallach D,  Goltsev Y,  Kovalenko A,  Varfolomeev E,  Brodianski V;
XX
DR   WPI; 1998-495842/42.
DR   N-PSDB; AAV52968.
XX
PT   New DNA encoding isoforms of G1 protein which bind MORT-1 - and regulate
PT   the effects of FAS and tumour necrosis factor receptors, useful for
PT   killing of cells e.g. HIV and cancer cells.
XX
PS   Claim 12; Fig 1B; 132pp; English.
XX
CC   This is the amino acid sequence of the alpha isoform of novel human G1
CC   protein. The sequence is deduced from an isolated skin fibroblast cDNA
CC   clone (see AAV52968). G1-alpha (also called CASH alpha, CASH being
CC   caspase homologue) and a shorter isoform, G1-beta (see AAW78904),
CC   represent 2 splice variants of the G1 protein. These G1 proteins are
CC   capable of binding to, or interacting directly or indirectly, via their N
CC   -terminal MORT modules, with MORT-1 or with MORT-binding proteins such as
CC   Mch4 (CASP-10) and MACH (CASP-8), and thereby of binding to the
CC   intracellular domain of the FAS-R receptor, to which MORT-1 binds, or of
CC   binding to the intracellular domain of the p55 tumour necrosis factor
CC   (TNF) receptor, to which TRADD binds and to which TRADD protein MORT-1
CC   binds. Hence, they are considered as mediators or modulators of FAS-R
CC   having a role in e.g. the signalling process that is initiated by the
CC   binding of FAS ligand to FAS-R, and also having a role in the signalling
CC   process initiated by the binding of TNF to p55-R. The longer isoform also
CC   has a C-terminal caspase activity region involved in cytotoxic activity.
CC   G1 DNA (I) and polypeptide (II), vectors and fragments are used to
CC   regulate cell death or inflammatory processes. (II) is used to inhibit
CC   cell death, and its inhibitors augment/enhance the processes. (I) and
CC   (II) regulate the FAS-R ligand or TNF effect on cells carrying an FAS-R
CC   or p55-R. Tumour, HIV-infected or other diseased cells can be treated
CC   using a viral vector encoding a viral surface protein, which binds a
CC   specific cell surface receptor and a sequence encoding (II), which kills
CC   the cell. Antisense oligonucleotides, introduced using the above vector,
CC   block the expression of (II) and can also regulate the above effects.
CC   These effects can also be regulated using a vector encoding a ribozyme
CC   that interacts with a cellular mRNA encoding (II), and allows (II)
CC   expression
XX
SQ   Sequence 480 AA;

  Query Match             96.7%;  Score 504;  DB 2;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 9.6e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 22
AAW76631
ID   AAW76631 standard; protein; 480 AA.
XX
AC   AAW76631;
XX
DT   12-JUL-1999  (first entry)
XX
DE   Human CFLIP-L protein.
XX
KW   Death effector domain; human; murine; anti-apoptotic; treatment;
KW   HIV infection; autoimmune disease; FLIP protein.
XX
OS   Homo sapiens.
XX
PN   DE19713393-A1.
XX
PD   08-OCT-1998.
XX
PF   01-APR-1997;   97DE-01013393.
XX
PR   01-APR-1997;   97DE-01013393.
```

```
XX
PA   (TSCH/) TSCHOPP J.
XX
PI   Tschopp J,  Thome M,  Burns K,  Irmler M,  Hahne M,  Schroeter M;
PI   Schneider P,  Bodmer J,  Steiner V,  Rimoldi D,  Hoffmann K,  French EL;
XX
DR   WPI; 1998-532710/46.
DR   N-PSDB; AAV61937.
XX
PT   New DNA encoding for anti-apoptotic gene product - used to treat HIV
PT   infections and autoimmune diseases.
XX
PS   Claim 20; Fig 4B; 45pp; German.
XX
CC   This invention describes novel human and mouse anti-apoptotic gene
CC   products which contain at least one death effector domain. The products
CC   of the invention are used in the treatment of HIV infections and
CC   autoimmune diseases
XX
SQ   Sequence 480 AA;

  Query Match             96.7%;  Score 504;  DB 2;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 9.6e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 23
AAY05787
ID   AAY05787 standard; protein; 480 AA.
XX
AC   AAY05787;
XX
DT   02-AUG-1999  (first entry)
XX
DE   Human MACH related inducer of toxicity MRIT alpha 1.
XX
KW   MRIT alpha 1; MACH related inducer of toxicity; human; apoptosis;
KW   pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis;
KW   atherosclerosis; neurodegenerative disease; Alzheimer's disease;
KW   Parkinson's disease; retinitis pigmentosa; stroke; AIDS;
KW   aplastic anaemia; myocardial infarction; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .165
FT                   /note= "death effector domain homology region"
FT   Region          140. .178
FT                   /note= "Bcl-2 homology region"
FT   Region          196. .228
FT                   /note= "Bcl-2 homology region"
FT   Region          258. .289
FT                   /note= "Bcl-2 homology region"
FT   Region          299. .350
FT                   /note= "Bcl-2 homology region"
FT   Region          301. .480
FT                   /note= "caspase homology region"
FT   Region          356. .397
FT                   /note= "Bcl-2 homology region"
FT   Active-site     358. .362
XX
PN   WO9918230-A2.
XX
PD   15-APR-1999.
XX
PF   07-OCT-1998;   98WO-US021132.
XX
PR   07-OCT-1997;   97US-00946226.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Chaudhary PM;
XX
DR   WPI; 1999-277275/23.
DR   N-PSDB; AAX25508.
XX
PT   Identifying regulators of MACH-related inducer of toxicity.
XX
PS   Example 1; Fig 1F; 78pp; English.
XX
CC   The present sequence represents novel human MACH-related inducer of
CC   toxicity (MRIT) isoform MRIT alpha 1, a CED-4 homologue that interacts
CC   simultaneously with caspases and Bcl-2 family polypeptides, and which has
CC   pro-apoptotic activity. Multiple isoforms of MRIT have been identified,
CC   some of which function to induce caspase dependent apoptosis in mammalian
CC   cells, e.g. MRIT alpha 1 and MRIT beta 1 (see AAY05789), while others
CC   have anti-apoptotic activity, e.g. MRIT alpha 2 (see AAY05788). MRIT
CC   alpha 1 includes an N-terminal death effector domain and a C-terminal
CC   caspase homology domain, but is not a cysteine protease. Selective
CC   enhancers and inhibitors of MRIT apoptotic activity can be identified and
CC   used to treat diseases mediated by the dysfunction of programmed cell
CC   death or proliferation. A cell accumulation disorder such as cancer,
CC   autoimmune disease, viral infection, angiogenesis or atherosclerosis is
CC   treated by administering an agent that selectively enhances MRIT
CC   apoptotic activity, thereby inducing apoptosis in a subject. A disorder
CC   of cell loss, such as a neurodegenerative disorder, including Alzheimer's
CC   disease, Parkinson's disease, retinitis pigmentosa, stroke, aplastic
CC   anaemia, myocardial infarction or AIDS can be treated by administering an
CC   agent that selectively inhibits MRIT apoptotic activity
XX
SQ   Sequence 480 AA;

  Query Match             96.7%;  Score 504;  DB 2;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 9.6e-51;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 24
AAY57454
ID   AAY57454 standard; protein; 480 AA.
XX
AC   AAY57454;
XX
DT   25-FEB-2000  (first entry)
XX
DE   Human FLICE-like inhibitory protein long form protein sequence.
XX
KW   Human; FLICE-like inhibitory protein long form; FLIP-L; FLIP-S;
KW   FLICE-like inhibitory protein short form; apoptosis inhibitor;
KW   arteriosclerosis; vascular wall inflammation; vascular injury;
KW   Fas ligand-mediated apoptosis; atherosclerosis; transplant.
XX
OS   Homo sapiens.
XX
PN   WO9942570-A1.
XX
PD   26-AUG-1999.
XX
PF   19-FEB-1999;   99WO-US003558.
XX
```

PR 20-FEB-1998; 98US-0075471P.
XX
PA (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
XX
PI Walsh K;
XX
DR WPI; 1999-527469/44.
DR N-PSDB; AAZ39040.
XX
PT Treating conditions characterized by vascular wall inflammation.
XX
PS Claim 5; Page 69-71; 105pp; English.
XX
CC The present sequence represents human FLICE-like inhibitory protein long
CC form, designated FLIP-L. The present invention describes a new treatment
CC of a condition characterised by vascular wall inflammation in a subject
CC comprising administering a FLIP molecule to inhibit Fas ligand-mediated
CC apoptosis of vascular endothelial cells in the subject. The method can be
CC used to treat atherosclerosis, transplant arteriosclerosis and vascular
CC injury
XX
SQ Sequence 480 AA;

Query Match 96.7%; Score 504; DB 2; Length 480;
Best Local Similarity 99.0%; Pred. No. 9.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy 64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
|||||||||||||||||||||||||||||||||||:||||
Db 61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 25
AAY59414
ID AAY59414 standard; protein; 480 AA.
XX
AC AAY59414;
XX
DT 21-MAR-2000 (first entry)
XX
DE Human CLARP protein sequence.
XX
KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;
KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;
KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;
KW aplastic anaemia; ischaemic injury; toxin-induced liver disease; CLARP.
XX
OS Homo sapiens.
XX
PN WO9955134-A2.
XX
PD 04-NOV-1999.
XX
PF 27-APR-1999; 99WO-US009183.
XX
PR 27-APR-1998; 98US-00069023.
XX
PA (UNMI) UNIV MICHIGAN.
XX
PI Nunez G, Inohara N, Koseki T;
XX
DR WPI; 2000-072163/06.
DR N-PSDB; AAZ48769.
XX
PT Compositions for identifying apoptosis signaling pathway inhibitors
PT useful for treating diseases.
XX
PS Example 10; Fig 21b; 93pp; English.
XX
CC This sequence is the human CLARP protein. The invention relates to the
CC human RICK (RIP-like interacting CLARP kinase) protein. The RICK protein
CC acts as a positive regulator of apoptosis, potentiating apoptosis induced
CC by caspase-8 and caspase-10 during CD95 signalling. The invention
CC provides methods for identifying apoptosis signalling pathway inhibitors
CC and activators, and methods and compositions for screening compounds
CC which will modulate the interactions of the various compositions
CC identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B
CC and DREP-1). RICK is useful in screening assays for agents, useful in the
CC diagnosis, prognosis or treatment of disease associated with excess cell
CC growth and dysregulation of apoptosis. Complexes containing RICK and
CC CLARP can be used in drug screening assays to identify inhibitor
CC molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an
CC in vitro cell system can be used to identify inhibitors of the enzymatic
CC activity of caspase-8. Identification of ARC-like inhibitory compounds
CC may be useful for gene therapy treatment of disease with increased cell
CC death in muscle tissue and cardiac disorders. Therapeutic compositions of
CC CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative
CC disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver
CC disease. AntiRICK antibodies can be used as reagents for the preparation
CC or affinity chromatography media, and for diagnostically measuring RICK
CC levels. A specific inhibitor of an essential step in the biochemistry of
CC apoptosis is needed. RICK interaction with intracellular factors such as
CC CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK
CC binding to intracellular apoptosis factors are potential drug candidates
XX
SQ Sequence 480 AA;

Query Match 96.7%; Score 504; DB 3; Length 480;
Best Local Similarity 99.0%; Pred. No. 9.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy 64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
|||||||||||||||||||||||||||||||||||:||||
Db 61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 26
AAY57606
ID AAY57606 standard; protein; 480 AA.
XX
AC AAY57606;
XX
DT 10-MAR-2000 (first entry)
XX
DE Human apoptosis associated protein HAPOP-1.
XX
KW Human; apoptosis associated protein; HAPOP; diagnosis; cytostatic;
KW antiarteriosclerotic; antiarthritic; hepatotropic; apoptosis regulator;
KW cell proliferative disorder; atherosclerosis; arteriosclerosis; cancer;
KW immune disorder; rheumatoid arthritis; systemic lupus erythematosus;
KW reproductive disorder; tumour; gastrointestinal disorder; cirrhosis;
KW colitis; hepatitis; pancreatitis.
XX
OS Homo sapiens.
XX
PN WO9958692-A2.
XX
PD 18-NOV-1999.
XX
PF 11-MAY-1999; 99WO-US010386.
XX
PR 13-MAY-1998; 98US-00078402.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Corley NC, Guegler KJ, Patterson C, Baughn M;
XX

DR WPI; 2000-062303/05.
DR N-PSDB; AAZ47926.
XX
PT New protein for diagnosing, treating or preventing disorders associated
PT with increased or decreased apoptosis.
XX
PS Claim 1; Page 70-71; 81pp; English.
XX
CC The present sequence represents a human apoptosis associated protein
CC designated HAPOP-1. HAPOP proteins are apoptosis regulators which have
CC antiarteriosclerotic, cytostatic, antiarthritic and hepatotropic
CC activity. A pharmaceutical composition comprising HAPOP in conjunction
CC with a carrier, a purified antagonist of HAPOP, vectors and agonists of
CC HAPOP, are administered for diagnosing, treating or preventing disorders
CC associated with increased or decreased apoptosis, e.g. cell proliferative
CC disorders such as atherosclerosis, arteriosclerosis and cancers; immune
CC disorders such as rheumatoid arthritis, systemic lupus erythematosus;
CC reproductive disorders such as prostate cancer, endometrial and ovarian
CC tumours; and gastrointestinal disorders such as cirrhosis, colitis,
CC hepatitis and pancreatitis. The polynucleotides encoding HAPOP proteins
CC may be useful to detect and quantitate expression of HAPOP genes which
CC are correlated with diseases and are also useful to detect differences in
CC the chromosomal location due to translocation, inversion etc., among
CC normal, carrier, or affected individuals. The combination of the
CC therapeutic agents may act synergistically to effect the treatment or
CC prevention of various disorders providing improved efficacy with lower
CC dosages of each agent and thus reducing the potential for adverse side
CC effects
XX
SQ Sequence 480 AA;

Query Match 96.7%; Score 504; DB 3; Length 480;
Best Local Similarity 99.0%; Pred. No. 9.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
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Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy 64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
|||||||||||||||||||||||||||||||||||||:||||
Db 61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 27
AAY67418
ID AAY67418 standard; protein; 480 AA.
XX
AC AAY67418;
XX
DT 12-MAY-2000 (first entry)
XX
DE Usurpin-alpha polypeptide.
XX
KW Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta;
KW usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
KW caspase; cytostatic; antiParkinsonian; antidiabetic.
XX
OS Homo sapiens.
XX
PN WO200003023-A1.
XX
PD 20-JAN-2000.
XX
PF 07-JUL-1999; 99WO-CA000615.
XX
PR 08-JUL-1998; 98US-0092005P.
XX
PA (MERI) MERCK FROSST CANADA INC.
XX
PI Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;
XX
DR WPI; 2000-160929/14.
DR N-PSDB; AAZ56987.
XX
PT Novel recombinant DNA molecules and polypeptides for treating apoptosis
PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
PT disease.
XX
PS Claim 6; Fig 9B; 69pp; English.
XX
CC The invention provides recombinant nucleic acid molecules encoding
CC usurpin-alpha (lacking the first death effector domain (DED) or its
CC prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are
CC useful for in vitro and in vivo identification of usurpin-procaspase-8
CC interaction inhibitor. Usurpin is useful as modulator of the sensitivity
CC of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
CC is useful for treating diseases like autoimmune diabetes, cancer and
CC Parkinson's disease. Activators and inhibitors of usurpin-procaspase-8
CC interaction are also useful for treating various diseases mediated by
CC apoptosis. Usurpin provides an attractive model for modulating caspase
CC activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be
CC regulated at several levels in the presence of usurpin, conferring
CC resistance to Fas-ligand cell death. The present sequence represents the
CC usurpin-alpha polypeptide
XX
SQ Sequence 480 AA;

Query Match 96.7%; Score 504; DB 3; Length 480;
Best Local Similarity 99.0%; Pred. No. 9.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
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Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy 64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
|||||||||||||||||||||||||||||||||||||:||||
Db 61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 28
AAB03960
ID AAB03960 standard; protein; 480 AA.
XX
AC AAB03960;
XX
DT 26-FEB-2001 (first entry)
XX
DE FLICE-like inhibitor protein (Genbank Accession No. 2253679).
XX
KW Chimeric protein; fusion protein; FLICE like inhibitor protein; FLIP;
KW Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;
KW tumour specific antigen; immune response; therapy; prophylaxis;
KW diagnosis; HIV; human immunodeficiency syndrome; AIDS;
KW acquired immune deficiency syndrome; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200059935-A1.
XX
PD 12-OCT-2000.
XX
PF 05-APR-2000; 2000WO-US009002.
XX
PR 05-APR-1999; 99US-0127867P.
PR 06-APR-1999; 99US-0128021P.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PA (PAYA/) PAYA C.
PA (ALGE/) ALGECIRAS-SCHMINICH A.
XX
PI Paya C, Algeciras-Schminich A;
XX
DR WPI; 2000-664988/64.

XX
PT Fusion polypeptide useful for inhibiting ligand-induced apoptosis,
PT comprises portion of anti-apoptotic polypeptide linked to a transport
PT group.
XX
PS Disclosure; Page 79-81; 89pp; English.
XX
CC A chimeric group or fusion peptide which comprises a portion of an anti-
CC apoptotic polypeptide which inhibits apoptosis of lymphocytes in
CC combination with a transport group is described. The transport group is
CC capable of transporting the chimeric group or fusion peptide across the
CC cell membrane. The anti-apoptotic polypeptide is FLICE-like inhibitor
CC protein (FLIP) which inhibits Fas and TNF mediated apoptosis by
CC inhibiting binding of Caspase-8 to the Fas receptor complex, thus
CC shutting off the downstream Fas signalling pathway. The chimeric group
CC and fusion peptide are useful for inhibiting ligand-induced apoptosis by
CC bringing them into contact with T cells. The chimeric group is useful for
CC expanding T cells in vitro e.g. T cells specific for particular antigens
CC such as tumour-specific antigen, for enhancing immune response and to
CC inhibit the apoptosis of chronically activated T cells e.g. activated
CC CD4^+ T cells in HIV infected patients. The chimeric group is also useful
CC for therapeutic, prophylactic or diagnosis of intracellular delivery of
CC small molecules and macromolecules such as anti-apoptotic polypeptides
CC and nucleic acids encoding such polypeptides
XX
SQ Sequence 480 AA;

Query Match 96.7%; Score 504; DB 3; Length 480;
Best Local Similarity 99.0%; Pred. No. 9.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
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Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy 64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
|||||||||||||||||||||||||||||||||||||:||||
Db 61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 29
ABB09294
ID ABB09294 standard; protein; 480 AA.
XX
AC ABB09294;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human FLIP-c protein SEQ ID NO:11.
XX
KW Human; FLIP-c; caspase 8 dominant negative regulator; antiinflammatory;
KW anti-tumour; FLIP-c inhibitor; apoptosis; antisense gene therapy;
KW phosphorothioate; antisense modulation; infection; inflammation; tumour.
XX
OS Homo sapiens.
XX
PN WO200224717-A1.
XX
PD 28-MAR-2002.
XX
PF 14-SEP-2001; 2001WO-US028732.
XX
PR 20-SEP-2000; 2000US-00666269.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ackermann EJ, Bennett CF, Zhang H, Watt AT, Ricketts W, Dean NM;
XX
DR WPI; 2002-404948/43.
DR N-PSDB; ABL52333.
XX
PT Novel antisense compound that hybridizes and inhibits nucleic acid
PT encoding a natural dominant negative regulator of caspase 8, FLIP-c,
PT useful for preventing or delaying infection, inflammation or tumor
PT formation.
XX
PS Example 13; Page 118-120; 154pp; English.
XX
CC The present invention describes a compound (I) 8-50 nucleobases in length
CC targeted to a nucleic acid molecule (II) encoding a natural dominant
CC negative regulator of caspase 8, FLIP-c, where (I) specifically
CC hybridises with and inhibits expression of the protein, or specifically
CC hybridises with at least an 8-nucleobase portion of an active site on
CC (II). (I) has antiinflammatory and anti-tumour activities. (I) is an
CC inhibitor of FLIP-c expression, a modulator of apoptosis and can be used
CC in antisense gene therapy. (I) is useful for inhibiting the expression of
CC FLIP-c in cells or tissues, and for treating an animal having a disease
CC or condition associated with FLIP-c. (I) is also useful for modulating
CC apoptosis in a cell, where a caspase such as caspase 8, caspase 3 or
CC caspase 7 is activated, and the FLIP-c is the long form of FLIP-c. (I) is
CC also useful for diagnostics, therapeutics, prophylaxis, as research
CC reagents and kits, for distinguishing functions of various members of a
CC biological pathway, and in antisense gene therapy. (I) is also useful
CC prophylactically, e.g., to prevent or delay infection, inflammation or
CC tumour formation. The present sequence represents human FLIP-c as given
CC in an example from the present invention
XX
SQ Sequence 480 AA;

Query Match 96.7%; Score 504; DB 5; Length 480;
Best Local Similarity 99.0%; Pred. No. 9.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
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Db 61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 30
ADA10615
ID ADA10615 standard; protein; 480 AA.
XX
AC ADA10615;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human inhibitor of FLICE (I-FLICE-1) protein.
XX
KW Human; I-FLICE-1; inhibitor of FLICE; FADD-like ICE;
KW tumour necrosis factor receptor-1 inhibitor; TNFR-1 inhibitor;
KW CD-95 induced apoptosis; apoptosis associated disease;
KW Alzheimer's disease; rheumatoid arthritis; stroke; osteoporosis;
KW ischaemia; septic shock; degenerative liver disease;
KW cardiovascular disorder; aberrant cell survival; nootropic;
KW antirheumatic; vasotropic; hepatotropic; osteopathic; cardiant;
KW cerebroprotective; antibacterial; antiarthritic; vasodilator.
XX
OS Homo sapiens.
XX
PN US2003087339-A1.
XX
PD 08-MAY-2003.
XX
PF 21-JAN-1998; 98US-00009893.
XX
PR 21-JAN-1997; 97US-0034205P.
PR 05-AUG-1997; 97US-0054800P.
XX
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (DIXI/) DIXIT V M.
PA (GENT/) GENTZ R L.

PA (KENN/) KENNY J J.
XX
PI Ni J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;
XX
DR WPI; 2003-576674/54.
DR N-PSDB; ADA10614.
XX
PT New I-FLICE-1 (inhibitor of FLICE 1) or I-FLICE-2 nucleic acids, useful
PT for treating diseases associated with apoptosis e.g., Alzheimer's
PT disease, rheumatoid arthritis, stroke, osteoporosis, ischemia or septic
PT shock.
XX
PS Claim 1; Fig 1A-1B; 48pp; English.
XX
CC The present invention relates to the isolation of novel human I-FLICE-1
CC (inhibitor of FLICE (FADD-like ICE)) and I-FLICE-2 proteins, and the
CC polynucleotide sequences encoding them. The I-FLICE-1 and I-FLICE-2
CC proteins are novel inhibitors of tumour necrosis factor receptor-1 (TNFR-
CC 1) and CD-95 induced apoptosis. Also disclosed are vectors, host cells
CC and recombinant methods for producing the I-FLICE proteins. The sequences
CC and methods are useful for treating diseases associated with apoptosis
CC e.g. Alzheimer's disease, rheumatoid arthritis, stroke, osteoporosis,
CC ischaemia, septic shock, degenerative liver disease, and cardiovascular
CC disorders. They are also useful for diagnosing diseases or disorders
CC associated with aberrant cell survival in an individual. The present
CC sequence represents human I-FLICE-1.
XX
SQ Sequence 480 AA;

Query Match 96.7%; Score 504; DB 7; Length 480;
Best Local Similarity 99.0%; Pred. No. 9.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
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Search completed: September 30, 2005, 08:00:06
Job time : 74 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 30, 2005, 07:58:49 ; Search time 1888 Seconds
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Title: US-09-402-569-2
Perfect score: 521
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	504	96.7	221	9	US-09-410-194-15	Sequence 15, Appl
2	504	96.7	221	9	US-09-410-194-22	Sequence 22, Appl
3	504	96.7	221	16	US-10-849-901-4	Sequence 4, Appli
4	504	96.7	221	17	US-10-832-218-15	Sequence 15, Appl
5	504	96.7	221	17	US-10-832-218-22	Sequence 22, Appl
6	504	96.7	221	18	US-10-998-582-4	Sequence 4, Appli
7	504	96.7	445	9	US-09-935-223-2	Sequence 2, Appli
8	504	96.7	445	16	US-10-825-282-44	Sequence 44, Appl
9	504	96.7	462	16	US-10-755-889-102	Sequence 102, App
10	504	96.7	480	9	US-09-861-270-2	Sequence 2, Appli
11	504	96.7	480	9	US-09-410-194-11	Sequence 11, Appl
12	504	96.7	480	9	US-09-410-194-17	Sequence 17, Appl
13	504	96.7	480	10	US-09-009-893-2	Sequence 2, Appli
14	504	96.7	480	10	US-09-471-749-1	Sequence 1, Appli
15	504	96.7	480	16	US-10-408-765A-275	Sequence 275, App
16	504	96.7	480	16	US-10-713-208-2	Sequence 2, Appli
17	504	96.7	480	16	US-10-849-901-2	Sequence 2, Appli
18	504	96.7	480	17	US-10-832-218-11	Sequence 11, Appl
19	504	96.7	480	17	US-10-832-218-17	Sequence 17, Appl
20	504	96.7	480	18	US-10-998-582-2	Sequence 2, Appli
21	465	89.3	93	9	US-09-864-761-36370	Sequence 36370, A
22	390	74.9	481	9	US-09-410-194-12	Sequence 12, Appl
23	390	74.9	481	9	US-09-410-194-19	Sequence 19, Appl
24	390	74.9	481	17	US-10-832-218-12	Sequence 12, Appl
25	390	74.9	481	17	US-10-832-218-19	Sequence 19, Appl
26	390	74.9	484	13	US-10-005-921-2	Sequence 2, Appli
27	390	74.9	484	16	US-10-849-901-5	Sequence 5, Appli
28	390	74.9	484	18	US-10-998-582-5	Sequence 5, Appli
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31	129.5	24.9	188	9	US-09-410-194-23	Sequence 23, Appl
32	129.5	24.9	188	17	US-10-832-218-23	Sequence 23, Appl
33	121.5	23.3	169	9	US-09-410-194-5	Sequence 5, Appli
34	121.5	23.3	169	17	US-10-832-218-5	Sequence 5, Appli
35	119	22.8	165	9	US-09-410-194-6	Sequence 6, Appli
36	119	22.8	165	17	US-10-832-218-6	Sequence 6, Appli
37	114.5	22.0	482	18	US-10-627-556-458	Sequence 458, App
38	114.5	22.0	977	18	US-10-627-556-494	Sequence 494, App
39	114.5	22.0	977	18	US-10-627-556-496	Sequence 496, App
40	114.5	22.0	990	18	US-10-627-556-460	Sequence 460, App
41	114.5	22.0	990	18	US-10-627-556-462	Sequence 462, App
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44	105.5	20.2	182	9	US-09-410-194-24	Sequence 24, Appl
45	105.5	20.2	182	17	US-10-832-218-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-410-194-15
; Sequence 15, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-15

Query Match 96.7%; Score 504; DB 9; Length 221;

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RESULT 2
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; Sequence 22, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
;  APPLICANT: Tschopp, Jurg
;  APPLICANT:  Thome, Margot
;  APPLICANT:  Burns, Kimberly
;  APPLICANT:  Irmler, Marten
;  APPLICANT:  Hahne, Michael
;  APPLICANT:  Schroter, Michael
;  APPLICANT:  Schneider, Pascal
;  APPLICANT:  Bodmer, Jean- Luc
;  APPLICANT:  Steiner, Veronique
;  APPLICANT:  Rimoldi, Donata
;  APPLICANT:  Hofmann, Kay
;  APPLICANT:  French, E. Lars
;  TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
;  FILE REFERENCE: 11141-002001
;  CURRENT APPLICATION NUMBER: US/09/410,194
;  CURRENT FILING DATE:  1999-09-30
;  PRIOR APPLICATION NUMBER: PCT/EP98/01857
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 221
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-410-194-22

  Query Match             96.7%;  Score 504;  DB 9;  Length 221;
  Best Local Similarity   99.0%;  Pred. No. 1.6e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 3
US-10-849-901-4
; Sequence 4, Application US/10849901
; Publication No. US20040230039A1
; GENERAL INFORMATION:
;  APPLICANT: WALLACH, David
;  APPLICANT:  GOLTSEV, Yura
;  APPLICANT:  KOVALENKO, Andrei
;  APPLICANT:  VARFOLOMEEV, Eugene
;  APPLICANT:  BRODIANSKI, Vadim
;  TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,
;  TITLE OF INVENTION:  MODULATORS OF THE FUNCTION OF FAS RECEPTORS
;  FILE REFERENCE: WALLACH=23
;  CURRENT APPLICATION NUMBER: US/10/849,901
;  CURRENT FILING DATE:  2004-05-21
;  PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/380,546
;  PRIOR FILING DATE: CURRENT FILING DATE:  1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/IL98/00098
;  PRIOR FILING DATE: 1998-02-26
;  PRIOR APPLICATION NUMBER: IL 120367
;  PRIOR FILING DATE: 1997-03-03
;  PRIOR APPLICATION NUMBER: IL120759
;  PRIOR FILING DATE: 1997-05-01
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 221
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-849-901-4

  Query Match             96.7%;  Score 504;  DB 16;  Length 221;
  Best Local Similarity   99.0%;  Pred. No. 1.6e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 4
US-10-832-218-15
; Sequence 15, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
;  APPLICANT: Tschopp, Jurg
;  APPLICANT:  Thome, Margot
;  APPLICANT:  Burns, Kimberly
;  APPLICANT:  Irmler, Marten
;  APPLICANT:  Hahne, Michael
;  APPLICANT:  Schroter, Michael
;  APPLICANT:  Schneider, Pascal
;  APPLICANT:  Bodmer, Jean- Luc
;  APPLICANT:  Steiner, Veronique
;  APPLICANT:  Rimoldi, Donata
;  APPLICANT:  Hofmann, Kay
;  APPLICANT:  French, E. Lars
;  TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
;  FILE REFERENCE: 11141-002001
;  CURRENT APPLICATION NUMBER: US/10/832,218
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: US/09/410,194
;  PRIOR FILING DATE: 1999-09-30
;  PRIOR APPLICATION NUMBER: PCT/EP98/01857
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 221
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-832-218-15

  Query Match             96.7%;  Score 504;  DB 17;  Length 221;
  Best Local Similarity   99.0%;  Pred. No. 1.6e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
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                    ||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
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RESULT 5
US-10-832-218-22
; Sequence 22, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/10/832,218
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US/09/410,194
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-832-218-22

Query Match 96.7%; Score 504; DB 17; Length 221;
Best Local Similarity 99.0%; Pred. No. 1.6e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              ||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
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RESULT 6
US-10-998-582-4
; Sequence 4, Application US/10998582
; Publication No. US20050152877A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: GOLTSEV, Yura
; APPLICANT: KOVALENKO, Andrei
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: BRODIANSKI, Vadim
; TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; FILE REFERENCE: WALLACH=23
; CURRENT APPLICATION NUMBER: US/10/998,582
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US/09/380,546
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/IL98/00098
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: IL 120367
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: IL120759
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-998-582-4

Query Match 96.7%; Score 504; DB 18; Length 221;
Best Local Similarity 99.0%; Pred. No. 1.6e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              ||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
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RESULT 7
US-09-935-223-2
; Sequence 2, Application US/09935223
; Publication No. US20020086983A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, And
; TITLE OF INVENTION: Compositions For And Methods Of Making The Same
; FILE REFERENCE: TJU2499
; CURRENT APPLICATION NUMBER: US/09/935,223
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 09/723,450
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/276,993
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/859,167
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Novel Sequence
US-09-935-223-2

Query Match 96.7%; Score 504; DB 9; Length 445;
Best Local Similarity 99.0%; Pred. No. 3.7e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              ||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
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RESULT 8
US-10-825-282-44
; Sequence 44, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282

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;  CURRENT FILING DATE:  2004-04-14
;  PRIOR APPLICATION NUMBER: US/09/456,357
;  PRIOR FILING DATE: 1999-12-08
;  PRIOR APPLICATION NUMBER: 60/134,416
;  PRIOR FILING DATE: 1999-05-17
;  PRIOR APPLICATION NUMBER: 09/087,195
;  PRIOR FILING DATE: 1998-05-29
;  PRIOR APPLICATION NUMBER: 08/378,507
;  PRIOR FILING DATE: 1995-01-26
;  PRIOR APPLICATION NUMBER: 08/250,478
;  PRIOR FILING DATE: 1994-05-27
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
;   LENGTH: 445
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-825-282-44

  Query Match             96.7%;  Score 504;  DB 16;  Length 445;
  Best Local Similarity   99.0%;  Pred. No. 3.7e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 9
US-10-755-889-102
; Sequence 102, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
;  TITLE OF INVENTION:  PATHWAY
;  FILE REFERENCE: D0284 NP
;  CURRENT APPLICATION NUMBER: US/10/755,889
;  CURRENT FILING DATE:  2004-01-13
;  PRIOR APPLICATION NUMBER: U.S. 60/440,068
;  PRIOR FILING DATE: 2003-01-14
;  PRIOR APPLICATION NUMBER: U.S. 60/469,757
;  PRIOR FILING DATE: 2003-05-12
;  NUMBER OF SEQ ID NOS: 823
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 102
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-755-889-102

  Query Match             96.7%;  Score 504;  DB 16;  Length 462;
  Best Local Similarity   99.0%;  Pred. No. 3.9e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 10
US-09-861-270-2
; Sequence 2, Application US/09861270
; Patent No. US20020052474A1
;   GENERAL INFORMATION:
;        APPLICANT: Sul, Hong-Bing
;                   Goeddel, David V.
;        TITLE OF INVENTION: Regulators of Apoptosis
;        NUMBER OF SEQUENCES: 3
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Science & Technology Law Group
;             STREET: 75 Denise Drive
;             CITY: Hillsborough
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94010
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/861,270
;             FILING DATE: 18-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/795,088
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Osman, Richard A
;             REGISTRATION NUMBER: 36,627
;             REFERENCE/DOCKET NUMBER: T97-001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (650) 343-4341
;             TELEFAX: (650) 343-4342
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 480 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: not relevant
;             TOPOLOGY: not relevant
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-861-270-2

  Query Match             96.7%;  Score 504;  DB 9;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 4.1e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 11
US-09-410-194-11
; Sequence 11, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
;  APPLICANT: Tschopp, Jurg
;  APPLICANT:  Thome, Margot
;  APPLICANT:  Burns, Kimberly
;  APPLICANT:  Irmler, Marten
;  APPLICANT:  Hahne, Michael
;  APPLICANT:  Schroter, Michael
;  APPLICANT:  Schneider, Pascal
;  APPLICANT:  Bodmer, Jean- Luc
;  APPLICANT:  Steiner, Veronique
;  APPLICANT:  Rimoldi, Donata
;  APPLICANT:  Hofmann, Kay
;  APPLICANT:  French, E. Lars
;  TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
;  FILE REFERENCE: 11141-002001
;  CURRENT APPLICATION NUMBER: US/09/410,194
```

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;  CURRENT FILING DATE:  1999-09-30
;  PRIOR APPLICATION NUMBER: PCT/EP98/01857
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 480
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-410-194-11

  Query Match             96.7%;  Score 504;  DB 9;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 4.1e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 12
US-09-410-194-17
; Sequence 17, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
;  APPLICANT: Tschopp, Jurg
;  APPLICANT:  Thome, Margot
;  APPLICANT:  Burns, Kimberly
;  APPLICANT:  Irmler, Marten
;  APPLICANT:  Hahne, Michael
;  APPLICANT:  Schroter, Michael
;  APPLICANT:  Schneider, Pascal
;  APPLICANT:  Bodmer, Jean- Luc
;  APPLICANT:  Steiner, Veronique
;  APPLICANT:  Rimoldi, Donata
;  APPLICANT:  Hofmann, Kay
;  APPLICANT:  French, E. Lars
;  TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
;  FILE REFERENCE: 11141-002001
;  CURRENT APPLICATION NUMBER: US/09/410,194
;  CURRENT FILING DATE:  1999-09-30
;  PRIOR APPLICATION NUMBER: PCT/EP98/01857
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 480
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-410-194-17

  Query Match             96.7%;  Score 504;  DB 9;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 4.1e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 13
US-09-009-893-2
; Sequence 2, Application US/09009893
; Publication No. US20030087339A1
;  GENERAL INFORMATION:
;    APPLICANT:  NI, JIAN
;    APPLICANT:  ROSEN, CRAIG A.
;    APPLICANT:  DIXIT, VISHVA M.
;    APPLICANT:  GENTZ, REINER L.
;    APPLICANT:  KENNY, JOSEPH J.
;    TITLE OF INVENTION:  I-FLICE, A NOVEL INHIBITOR OF TUMOR
;    TITLE OF INVENTION:  NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  US
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/009,893
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/034,205
;      FILING DATE:  21-JAN-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/054,800
;      FILING DATE:  05-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEFFE, ERIC K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0970002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  480 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-009-893-2

  Query Match             96.7%;  Score 504;  DB 10;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 4.1e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 14
US-09-471-749-1
; Sequence 1, Application US/09471749
; Publication No. US20030124113A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Corley, Neil C.
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Patterson, Chandra
;    APPLICANT:  Baughn, Mariah
;    TITLE OF INVENTION:  HUMAN APOPTOSIS ASSOCIATED PROTEINS
```

```
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/471,749
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/078,402
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cerrone, Michael C.
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PF-0519 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  480 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  THP1PLB02
;      CLONE:  157658
US-09-471-749-1

  Query Match             96.7%;  Score 504;  DB 10;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 4.1e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 15
US-10-408-765A-275
; Sequence 275, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
;  APPLICANT: Ghosh, Soumitra S.
;  APPLICANT:  Fahy, Eoin D.
;  APPLICANT:  Zhang, Bing
;  APPLICANT:  Gibson, Bradford W.
;  APPLICANT:  Taylor, Steven W.
;  APPLICANT:  Glenn, Gary M.
;  APPLICANT:  Warnock, Dale E.
;  TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;  TITLE OF INVENTION:  IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;  FILE REFERENCE: 660088.465
;  CURRENT APPLICATION NUMBER: US/10/408,765A
;  CURRENT FILING DATE:  2003-04-04
;  NUMBER OF SEQ ID NOS: 3077
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 275
;   LENGTH: 480
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-765A-275

  Query Match             96.7%;  Score 504;  DB 16;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 4.1e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 16
US-10-713-208-2
; Sequence 2, Application US/10713208
; Publication No. US20040121387A1
; GENERAL INFORMATION:
;  APPLICANT: Ni et al.
;  TITLE OF INVENTION: I-FLICE, A Novel Inhibitor of Tumor Necrosis Factor Receptor-1 and
;  TITLE OF INVENTION:  CD-95 Induced Apoptosis
;  FILE REFERENCE: PF381C1D1
;  CURRENT APPLICATION NUMBER: US/10/713,208
;  CURRENT FILING DATE:  2003-11-17
;  PRIOR APPLICATION NUMBER: US 09/489,155
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/009,893
;  PRIOR FILING DATE: 1998-01-21
;  PRIOR APPLICATION NUMBER: US 60/054,800
;  PRIOR FILING DATE: 1997-08-05
;  PRIOR APPLICATION NUMBER: US 60/034,205
;  PRIOR FILING DATE: 1997-01-21
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 480
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-713-208-2

  Query Match             96.7%;  Score 504;  DB 16;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 4.1e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 17
US-10-849-901-2
; Sequence 2, Application US/10849901
; Publication No. US20040230039A1
; GENERAL INFORMATION:
;  APPLICANT: WALLACH, David
;  APPLICANT:  GOLTSEV, Yura
;  APPLICANT:  KOVALENKO, Andrei
;  APPLICANT:  VARFOLOMEEV, Eugene
;  APPLICANT:  BRODIANSKI, Vadim
;  TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,
;  TITLE OF INVENTION:  MODULATORS OF THE FUNCTION OF FAS RECEPTORS
;  FILE REFERENCE: WALLACH=23
;  CURRENT APPLICATION NUMBER: US/10/849,901
;  CURRENT FILING DATE:  2004-05-21
;  PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/380,546
;  PRIOR FILING DATE: CURRENT FILING DATE:  1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/IL98/00098
```

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;  PRIOR FILING DATE: 1998-02-26
;  PRIOR APPLICATION NUMBER: IL 120367
;  PRIOR FILING DATE: 1997-03-03
;  PRIOR APPLICATION NUMBER: IL120759
;  PRIOR FILING DATE: 1997-05-01
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 480
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-849-901-2

  Query Match             96.7%;  Score 504;  DB 16;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 4.1e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 18
US-10-832-218-11
; Sequence 11, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
;  APPLICANT: Tschopp, Jurg
;  APPLICANT:  Thome, Margot
;  APPLICANT:  Burns, Kimberly
;  APPLICANT:  Irmler, Marten
;  APPLICANT:  Hahne, Michael
;  APPLICANT:  Schroter, Michael
;  APPLICANT:  Schneider, Pascal
;  APPLICANT:  Bodmer, Jean- Luc
;  APPLICANT:  Steiner, Veronique
;  APPLICANT:  Rimoldi, Donata
;  APPLICANT:  Hofmann, Kay
;  APPLICANT:  French, E. Lars
;  TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
;  FILE REFERENCE: 11141-002001
;  CURRENT APPLICATION NUMBER: US/10/832,218
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: US/09/410,194
;  PRIOR FILING DATE: 1999-09-30
;  PRIOR APPLICATION NUMBER: PCT/EP98/01857
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 480
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-832-218-11

  Query Match             96.7%;  Score 504;  DB 17;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 4.1e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 19
US-10-832-218-17
; Sequence 17, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
;  APPLICANT: Tschopp, Jurg
;  APPLICANT:  Thome, Margot
;  APPLICANT:  Burns, Kimberly
;  APPLICANT:  Irmler, Marten
;  APPLICANT:  Hahne, Michael
;  APPLICANT:  Schroter, Michael
;  APPLICANT:  Schneider, Pascal
;  APPLICANT:  Bodmer, Jean- Luc
;  APPLICANT:  Steiner, Veronique
;  APPLICANT:  Rimoldi, Donata
;  APPLICANT:  Hofmann, Kay
;  APPLICANT:  French, E. Lars
;  TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
;  FILE REFERENCE: 11141-002001
;  CURRENT APPLICATION NUMBER: US/10/832,218
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: US/09/410,194
;  PRIOR FILING DATE: 1999-09-30
;  PRIOR APPLICATION NUMBER: PCT/EP98/01857
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 480
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-832-218-17

  Query Match             96.7%;  Score 504;  DB 17;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 4.1e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 20
US-10-998-582-2
; Sequence 2, Application US/10998582
; Publication No. US20050152877A1
; GENERAL INFORMATION:
;  APPLICANT: WALLACH, David
;  APPLICANT:  GOLTSEV, Yura
;  APPLICANT:  KOVALENKO, Andrei
;  APPLICANT:  VARFOLOMEEV, Eugene
;  APPLICANT:  BRODIANSKI, Vadim
;  TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,
;  TITLE OF INVENTION:  MODULATORS OF THE FUNCTION OF FAS RECEPTORS
;  FILE REFERENCE: WALLACH=23
;  CURRENT APPLICATION NUMBER: US/10/998,582
;  CURRENT FILING DATE:  2004-11-30
;  PRIOR APPLICATION NUMBER: US/09/380,546
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/IL98/00098
;  PRIOR FILING DATE: 1998-02-26
;  PRIOR APPLICATION NUMBER: IL 120367
;  PRIOR FILING DATE: 1997-03-03
;  PRIOR APPLICATION NUMBER: IL120759
;  PRIOR FILING DATE: 1997-05-01
;  NUMBER OF SEQ ID NOS: 20
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;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 480
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-998-582-2

  Query Match             96.7%;  Score 504;  DB 18;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 4.1e-47;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 21
US-09-864-761-36370
; Sequence 36370, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36370
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC007272.2
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL =   8
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL =   2
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.9
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =   2
;   OTHER INFORMATION: SWISSPROT HIT: Q66674, EVALUE 3.00e-04
;   OTHER INFORMATION: EST_HUMAN HIT: W23795.1, EVALUE 2.00e-46
US-09-864-761-36370

  Query Match             89.3%;  Score 465;  DB 9;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-43;
  Matches   93;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDY 96
              |||||||||||||||||||||||||||||||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDY 93


RESULT 22
US-09-410-194-12
; Sequence 12, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
;  APPLICANT: Tschopp, Jurg
;  APPLICANT:  Thome, Margot
;  APPLICANT:  Burns, Kimberly
;  APPLICANT:  Irmler, Marten
;  APPLICANT:  Hahne, Michael
;  APPLICANT:  Schroter, Michael
;  APPLICANT:  Schneider, Pascal
;  APPLICANT:  Bodmer, Jean- Luc
;  APPLICANT:  Steiner, Veronique
;  APPLICANT:  Rimoldi, Donata
;  APPLICANT:  Hofmann, Kay
;  APPLICANT:  French, E. Lars
;  TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
;  FILE REFERENCE: 11141-002001
;  CURRENT APPLICATION NUMBER: US/09/410,194
;  CURRENT FILING DATE:  1999-09-30
;  PRIOR APPLICATION NUMBER: PCT/EP98/01857
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 481
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-410-194-12

  Query Match             74.9%;  Score 390;  DB 9;  Length 481;
  Best Local Similarity   75.2%;  Pred. No. 1.7e-34;
  Matches   79;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 60
              :| :|||||||||| || |||||:|||||||  ::  |||||||| | |||:||   |||
Db          3 QSPVSAEVIHQVEECLDEDEKEMMLFLCRDVTENLAAPNVRDLLDSLSERGQLSFATLAE 62
```

```
Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              ||||||||||||||| |:  || || ||||||||||||: ||||
Db         63 LLYRVRRFDLLKRILKTDKATVEDHLRRNPHLVSDYRVLLMEIGE 107


RESULT 23
US-09-410-194-19
; Sequence 19, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
;  APPLICANT: Tschopp, Jurg
;  APPLICANT:  Thome, Margot
;  APPLICANT:  Burns, Kimberly
;  APPLICANT:  Irmler, Marten
;  APPLICANT:  Hahne, Michael
;  APPLICANT:  Schroter, Michael
;  APPLICANT:  Schneider, Pascal
;  APPLICANT:  Bodmer, Jean- Luc
;  APPLICANT:  Steiner, Veronique
;  APPLICANT:  Rimoldi, Donata
;  APPLICANT:  Hofmann, Kay
;  APPLICANT:  French, E. Lars
;  TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
;  FILE REFERENCE: 11141-002001
;  CURRENT APPLICATION NUMBER: US/09/410,194
;  CURRENT FILING DATE:  1999-09-30
;  PRIOR APPLICATION NUMBER: PCT/EP98/01857
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 481
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-410-194-19

  Query Match             74.9%;  Score 390;  DB 9;  Length 481;
  Best Local Similarity   75.2%;  Pred. No. 1.7e-34;
  Matches   79;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 60
              :| :|||||||||| || |||||:|||||||  ::  |||||||| | |||:||   |||
Db          3 QSPVSAEVIHQVEECLDEDEKEMMLFLCRDVTENLAAPNVRDLLDSLSERGQLSFATLAE 62

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              ||||||||||||||| |:  || || ||||||||||||: ||||
Db         63 LLYRVRRFDLLKRILKTDKATVEDHLRRNPHLVSDYRVLLMEIGE 107


RESULT 24
US-10-832-218-12
; Sequence 12, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
;  APPLICANT: Tschopp, Jurg
;  APPLICANT:  Thome, Margot
;  APPLICANT:  Burns, Kimberly
;  APPLICANT:  Irmler, Marten
;  APPLICANT:  Hahne, Michael
;  APPLICANT:  Schroter, Michael
;  APPLICANT:  Schneider, Pascal
;  APPLICANT:  Bodmer, Jean- Luc
;  APPLICANT:  Steiner, Veronique
;  APPLICANT:  Rimoldi, Donata
;  APPLICANT:  Hofmann, Kay
;  APPLICANT:  French, E. Lars
;  TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
;  FILE REFERENCE: 11141-002001
;  CURRENT APPLICATION NUMBER: US/10/832,218
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: US/09/410,194
;  PRIOR FILING DATE: 1999-09-30
;  PRIOR APPLICATION NUMBER: PCT/EP98/01857
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 481
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-832-218-12

  Query Match             74.9%;  Score 390;  DB 17;  Length 481;
  Best Local Similarity   75.2%;  Pred. No. 1.7e-34;
  Matches   79;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 60
              :| :|||||||||| || |||||:|||||||  ::  |||||||| | |||:||   |||
Db          3 QSPVSAEVIHQVEECLDEDEKEMMLFLCRDVTENLAAPNVRDLLDSLSERGQLSFATLAE 62

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              ||||||||||||||| |:  || || ||||||||||||: ||||
Db         63 LLYRVRRFDLLKRILKTDKATVEDHLRRNPHLVSDYRVLLMEIGE 107


RESULT 25
US-10-832-218-19
; Sequence 19, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
;  APPLICANT: Tschopp, Jurg
;  APPLICANT:  Thome, Margot
;  APPLICANT:  Burns, Kimberly
;  APPLICANT:  Irmler, Marten
;  APPLICANT:  Hahne, Michael
;  APPLICANT:  Schroter, Michael
;  APPLICANT:  Schneider, Pascal
;  APPLICANT:  Bodmer, Jean- Luc
;  APPLICANT:  Steiner, Veronique
;  APPLICANT:  Rimoldi, Donata
;  APPLICANT:  Hofmann, Kay
;  APPLICANT:  French, E. Lars
;  TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
;  FILE REFERENCE: 11141-002001
;  CURRENT APPLICATION NUMBER: US/10/832,218
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: US/09/410,194
;  PRIOR FILING DATE: 1999-09-30
;  PRIOR APPLICATION NUMBER: PCT/EP98/01857
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 481
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-832-218-19

  Query Match             74.9%;  Score 390;  DB 17;  Length 481;
  Best Local Similarity   75.2%;  Pred. No. 1.7e-34;
  Matches   79;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 60
              :| :|||||||||| || |||||:|||||||  ::  |||||||| | |||:||   |||
Db          3 QSPVSAEVIHQVEECLDEDEKEMMLFLCRDVTENLAAPNVRDLLDSLSERGQLSFATLAE 62

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              ||||||||||||||| |:  || || ||||||||||||: ||||
Db         63 LLYRVRRFDLLKRILKTDKATVEDHLRRNPHLVSDYRVLLMEIGE 107
```

```
RESULT 26
US-10-005-921-2
; Sequence 2, Application US/10005921
; Publication No. US20020174450A1
; GENERAL INFORMATION:
;  APPLICANT: Allen, Keith D.
;  APPLICANT:  Leviten, Michael W.
;  TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CASH GENE
;  TITLE OF INVENTION:  DISRUPTIONS
;  FILE REFERENCE: R-714
;  CURRENT APPLICATION NUMBER: US/10/005,921
;  CURRENT FILING DATE:  2001-12-04
;  PRIOR APPLICATION NUMBER: US 60/254,902
;  PRIOR FILING DATE: 2000-12-11
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 484
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-005-921-2

  Query Match             74.9%;  Score 390;  DB 13;  Length 484;
  Best Local Similarity   75.2%;  Pred. No. 1.7e-34;
  Matches   79;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 60
              :| :|||||||||| || |||||:|||||||  ::  |||||||| | |||:||   |||
Db          3 QSPVSAEVIHQVEECLDEDEKEMMLFLCRDVTENLAAPNVRDLLDSLSERGQLSFATLAE 62

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||| |:  || || ||||||||||: ||||
Db         63 LLYRVRRFDLLKRILKTDKATVEDHLRRNPHLVSDYRVLLMEIGE 107


RESULT 27
US-10-849-901-5
; Sequence 5, Application US/10849901
; Publication No. US20040230039A1
; GENERAL INFORMATION:
;  APPLICANT: WALLACH, David
;  APPLICANT:  GOLTSEV, Yura
;  APPLICANT:  KOVALENKO, Andrei
;  APPLICANT:  VARFOLOMEEV, Eugene
;  APPLICANT:  BRODIANSKI, Vadim
;  TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,
;  TITLE OF INVENTION:  MODULATORS OF THE FUNCTION OF FAS RECEPTORS
;  FILE REFERENCE: WALLACH=23
;  CURRENT APPLICATION NUMBER: US/10/849,901
;  CURRENT FILING DATE:  2004-05-21
;  PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/380,546
;  PRIOR FILING DATE: CURRENT FILING DATE:  1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/IL98/00098
;  PRIOR FILING DATE: 1998-02-26
;  PRIOR APPLICATION NUMBER: IL 120367
;  PRIOR FILING DATE: 1997-03-03
;  PRIOR APPLICATION NUMBER: IL120759
;  PRIOR FILING DATE: 1997-05-01
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 484
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-849-901-5

  Query Match             74.9%;  Score 390;  DB 16;  Length 484;
  Best Local Similarity   75.2%;  Pred. No. 1.7e-34;
  Matches   79;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 60
              :| :|||||||||| || |||||:|||||||  ::  |||||||| | |||:||   |||
Db          3 QSPVSAEVIHQVEECLDEDEKEMMLFLCRDVTENLAAPNVRDLLDSLSERGQLSFATLAE 62

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||| |:  || || ||||||||||: ||||
Db         63 LLYRVRRFDLLKRILKTDKATVEDHLRRNPHLVSDYRVLLMEIGE 107


RESULT 28
US-10-998-582-5
; Sequence 5, Application US/10998582
; Publication No. US20050152877A1
; GENERAL INFORMATION:
;  APPLICANT: WALLACH, David
;  APPLICANT:  GOLTSEV, Yura
;  APPLICANT:  KOVALENKO, Andrei
;  APPLICANT:  VARFOLOMEEV, Eugene
;  APPLICANT:  BRODIANSKI, Vadim
;  TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,
;  TITLE OF INVENTION:  MODULATORS OF THE FUNCTION OF FAS RECEPTORS
;  FILE REFERENCE: WALLACH=23
;  CURRENT APPLICATION NUMBER: US/10/998,582
;  CURRENT FILING DATE:  2004-11-30
;  PRIOR APPLICATION NUMBER: US/09/380,546
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/IL98/00098
;  PRIOR FILING DATE: 1998-02-26
;  PRIOR APPLICATION NUMBER: IL 120367
;  PRIOR FILING DATE: 1997-03-03
;  PRIOR APPLICATION NUMBER: IL120759
;  PRIOR FILING DATE: 1997-05-01
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 484
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-998-582-5

  Query Match             74.9%;  Score 390;  DB 18;  Length 484;
  Best Local Similarity   75.2%;  Pred. No. 1.7e-34;
  Matches   79;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 60
              :| :|||||||||| || |||||:|||||||  ::  |||||||| | |||:||   |||
Db          3 QSPVSAEVIHQVEECLDEDEKEMMLFLCRDVTENLAAPNVRDLLDSLSERGQLSFATLAE 62

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||| |:  || || ||||||||||: ||||
Db         63 LLYRVRRFDLLKRILKTDKATVEDHLRRNPHLVSDYRVLLMEIGE 107


RESULT 29
US-09-410-194-2
; Sequence 2, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
;  APPLICANT: Tschopp, Jurg
;  APPLICANT:  Thome, Margot
;  APPLICANT:  Burns, Kimberly
;  APPLICANT:  Irmler, Marten
;  APPLICANT:  Hahne, Michael
;  APPLICANT:  Schroter, Michael
;  APPLICANT:  Schneider, Pascal
;  APPLICANT:  Bodmer, Jean- Luc
;  APPLICANT:  Steiner, Veronique
;  APPLICANT:  Rimoldi, Donata
;  APPLICANT:  Hofmann, Kay
;  APPLICANT:  French, E. Lars
;  TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
;  FILE REFERENCE: 11141-002001
;  CURRENT APPLICATION NUMBER: US/09/410,194
;  CURRENT FILING DATE:  1999-09-30
;  PRIOR APPLICATION NUMBER: PCT/EP98/01857
```

```
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Humanes herpesvirus 8
US-09-410-194-2

  Query Match             24.9%;  Score 129.5;  DB 9;  Length 169;
  Best Local Similarity   34.0%;  Pred. No. 3.4e-06;
  Matches   35;  Conservative   23;  Mismatches   38;  Indels    7;  Gaps    3;

Qy          7 EVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILR---ERGKLSVGDLAELLY 63
              ||: :|   | ||::|::|||   : : :  | :  |:  ||   | |:|:   ||| |:
Db          5 EVLCEVARKLGTDDREVVLFL---LNVFIPQPTLAQLIGALRALKEEGRLTFPLLAECLF 61

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEI-GE 105
              |  | |||: :| :| : :| ||       | |:: :  : ||
Db         62 RAGRRDLLRDLLHLDPRFLERHLAGTMSYFSPYQLTVLHVDGE 104


RESULT 30
US-10-832-218-2
; Sequence 2, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
;  APPLICANT: Tschopp, Jurg
;  APPLICANT:  Thome, Margot
;  APPLICANT:  Burns, Kimberly
;  APPLICANT:  Irmler, Marten
;  APPLICANT:  Hahne, Michael
;  APPLICANT:  Schroter, Michael
;  APPLICANT:  Schneider, Pascal
;  APPLICANT:  Bodmer, Jean- Luc
;  APPLICANT:  Steiner, Veronique
;  APPLICANT:  Rimoldi, Donata
;  APPLICANT:  Hofmann, Kay
;  APPLICANT:  French, E. Lars
;  TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
;  FILE REFERENCE: 11141-002001
;  CURRENT APPLICATION NUMBER: US/10/832,218
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: US/09/410,194
;  PRIOR FILING DATE: 1999-09-30
;  PRIOR APPLICATION NUMBER: PCT/EP98/01857
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Humanes herpesvirus 8
US-10-832-218-2

  Query Match             24.9%;  Score 129.5;  DB 17;  Length 169;
  Best Local Similarity   34.0%;  Pred. No. 3.4e-06;
  Matches   35;  Conservative   23;  Mismatches   38;  Indels    7;  Gaps    3;

Qy          7 EVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILR---ERGKLSVGDLAELLY 63
              ||: :|   | ||::|::|||   : : :  | :  |:  ||   | |:|:   ||| |:
Db          5 EVLCEVARKLGTDDREVVLFL---LNVFIPQPTLAQLIGALRALKEEGRLTFPLLAECLF 61

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEI-GE 105
              |  | |||: :| :| : :| ||       | |:: :  : ||
Db         62 RAGRRDLLRDLLHLDPRFLERHLAGTMSYFSPYQLTVLHVDGE 104


Search completed: September 30, 2005, 08:34:18

Job time : 1889 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 30, 2005, 07:58:48 ; Search time 39 Seconds
(without alignments)
259.045 Million cell updates/sec

Title: US-09-402-569-2
Perfect score: 521
Sequence: 1 KSRMSAEVIHQVEEALDTDE.....LLRNPHLVSDYRVLMSEIGE 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	121.5	23.3	241	2	T30761	hypothetical prote
2	119	22.8	371	2	T30762	hypothetical prote
3	99.5	19.1	171	2	S55668	hypothetical prote
4	83	15.9	208	2	A56912	FADD protein - hum
5	77.5	14.9	1207	2	A89822	RNA polymerase bet
6	77	14.8	312	2	D90198	transposase ISC123
7	77	14.8	319	2	D90350	transposase ISC123
8	77	14.8	319	2	E90466	transposase ISC123
9	77	14.8	917	2	T05430	hypothetical prote
10	75.5	14.5	1057	2	T10908	DNA-directed RNA p
11	75.5	14.5	1372	2	B71724	dna-directed RNA p
12	75.5	14.5	1399	2	G83112	DNA-directed RNA p
13	75	14.4	1401	2	G82336	DNA-directed RNA p
14	73.5	14.1	312	2	T37338	probable 35.9K pro
15	73.5	14.1	312	2	PN0121	I1L protein - vacc
16	73.5	14.1	312	2	E72157	L1L protein - vari
17	73.5	14.1	312	2	F42510	I1L protein - vacc
18	73.5	14.1	312	2	S33070	I1L protein - vari
19	73.5	14.1	472	2	T27903	hypothetical prote
20	73.5	14.1	1372	2	F97722	hypothetical prote
21	73.5	14.1	1690	2	S41467	DNA-directed RNA p
22	73	14.0	319	2	D90344	transposase ISC123
23	73	14.0	319	2	D90342	transposase ISC123
24	73	14.0	319	2	S74012	hypothetical prote
25	73	14.0	319	2	H90321	transposase ISC123
26	73	14.0	319	2	G90428	transposase ISC123
27	73	14.0	1533	2	T00344	hypothetical prote
28	72.5	13.9	346	1	I48157	protein kinase (EC
29	72.5	13.9	348	2	B84448	hypothetical prote
30	72.5	13.9	485	1	JC4998	IMP dehydrogenase
31	72	13.8	151	2	H84033	transcription regu
32	71.5	13.7	486	1	E71456	IMP dehydrogenase
33	71.5	13.7	953	2	T46913	hypothetical prote
34	71.5	13.7	1377	2	C70148	DNA-directed RNA p
35	71.5	13.7	2890	2	B71846	dna-directed RNA p
36	71.5	13.7	2890	2	F64669	DNA-directed RNA p
37	71	13.6	785	2	D69985	DNA mismatch repai
38	71	13.6	1149	2	S67099	DNA-directed RNA p
39	70.5	13.5	168	2	T01482	hypothetical prote
40	70.5	13.5	932	2	F84465	hypothetical prote
41	70.5	13.5	953	2	S13520	coat protein beta
42	70.5	13.5	1048	2	T23764	hypothetical prote
43	70.5	13.5	1199	2	G69698	RNA polymerase (be
44	70.5	13.5	1316	2	G70535	probable rpoC prot
45	70	13.4	327	2	S08055	hypothetical prote

ALIGNMENTS

RESULT 1
T30761
hypothetical protein 159L - Molluscum contagiosum virus 1
N;Alternate names: MC159L
C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T30761
R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host res
A;Reference number: Z20876; MUID:96325459; PMID:8670425
A;Accession: T30761
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-241 <SEN>
A;Cross-references: UNIPROT:Q98325; EMBL:U60315; PIDN:AAC55287.1
C;Genetics:
A;Note: MC159L

Query Match 23.3%; Score 121.5; DB 2; Length 241;
Best Local Similarity 36.5%; Pred. No. 0.00026;
Matches 35; Conservative 16; Mismatches 40; Indels 5; Gaps 3;

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Qy         10 HQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFD 69
              | :|| ||: |  :||||| | |        |    |  | :: ||::  | |:|| ::| |
Db         15 HLLEE-LDSHEDSLLLFLCHDAAPGCT--TVTQALCSLSQQRKLTLAALVEMLYVLQRMD 71

Qy         70 LLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||    : ::  |   |     :: || ||  :||
Db         72 LLKSRFGLSKEGAEQ--LLGTSFLTRYRKLMVCVGE 105
```

RESULT 2
T30762
hypothetical protein 160L - Molluscum contagiosum virus 1
N;Alternate names: MC160L
C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T30762
R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host res
A;Reference number: Z20876; MUID:96325459; PMID:8670425
A;Accession: T30762
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-371 <SEN>
A;Cross-references: UNIPROT:Q98326; EMBL:U60315; PIDN:AAC55288.1
C;Genetics:
A;Note: MC160L

Query Match 22.8%; Score 119; DB 2; Length 371;

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  Best Local Similarity   38.6%;  Pred. No. 0.00074;
  Matches   34;  Conservative   12;  Mismatches   38;  Indels    4;  Gaps    2;

Qy         16 LDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRIL 75
              ||  | |:| |||||||         | |  |: |  |::  :|||| :||||:||
Db         18 LDASEHEVLRFLCRDVA--PASKTAEDALRALQRRRLLTLSSMAELLCALRRFDVLKVRF 75

Qy         76 KMDRKAVETHLLRNPHLVSDYRVLMSEI 103
                | |:      |     :| ||: :: |
Db         76 GMTRECAGR--LLGHGFLSQYRLQVAAI 101


RESULT 3
S55668
hypothetical protein E8 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55668
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55668
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-171 <TEL>
A;Cross-references: UNIPROT:Q66674; GB:U20824; NID:g695172; PIDN:AAC13862.1; PID:g695247
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
C;Superfamily: equine herpesvirus 2 hypothetical protein E8

  Query Match            19.1%;  Score 99.5;  DB 2;  Length 171;
  Best Local Similarity   39.4%;  Pred. No. 0.022;
  Matches   26;  Conservative    8;  Mismatches   21;  Indels   11;  Gaps    2;

Qy         15 ALDTDEKEMLLFLCRDVAIDVVPPN------VRDLLDILRERGKLSVGDLAELLYRVRRF 68
              :|| || |  |:||||:       |       ||    | :   ||  :  |||:|| |
Db         12 SLDEDETETYLYLCRDLL-----KNKGEFQCTRDAFKFLSDYACLSAANQMELLFRVGRL 66

Qy         69 DLLKRI 74
              ||::||
Db         67 DLIRRI 72


RESULT 4
A56912
FADD protein - human
N;Alternate names: FAS-associating death domain containing protein FADD; mediator of rec
C;Species: Homo sapiens (man)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C;Accession: A56912; I38041
R;Chinnaiyan, A.M.; O'Rourke, K.; Tewari, M.; Dixit, V.M.
Cell 81, 505-512, 1995
A;Title: FADD, a novel death domain-containing protein, interacts with the death domain
A;Reference number: A56912; MUID:95277837; PMID:7538907
A;Accession: A56912
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-208 <CHI>
A;Cross-references: UNIPROT:Q13158; GB:U24231; NID:g809486; PIDN:AAA86517.1; PID:g809487
R;Boldin, M.P.; Varfolomeev, E.E.; Pancer, Z.; Mett, I.L.; Camonis, J.H.; Wallach, D.
J. Biol. Chem. 270, 7795-7798, 1995
A;Title: A novel protein that interacts with the death domain of Fas/APO1 contains a seq
A;Reference number: I38041; MUID:95229578; PMID:7536190
A;Accession: I38041
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-31,'V',33-208 <RES>
A;Cross-references: EMBL:X84709; NID:g791037; PIDN:CAA59197.1; PID:g791038
C;Genetics:
A;Gene: GDB:FADD; MORT1
A;Cross-references: GDB:1320394
C;Superfamily: receptor-induced toxicity mediator MORT1
C;Keywords: apoptosis

  Query Match            15.9%;  Score 83;  DB 2;  Length 208;
  Best Local Similarity   27.6%;  Pred. No. 0.99;
  Matches   29;  Conservative   18;  Mismatches   50;  Indels    8;  Gaps    3;

Qy          8 VIHQVEEALDTDEKEMLLFLCRDVA----IDVVPPNVRDLLDILRERGKLSVGD---LAE 60
              ::| |  :| : |    | |||        :: |   : ||  :| |:  |  |     | |
Db          7 LLHSVSSSLSSSELTELKFLCLGRVGKRKLERVQSGL-DLFSMLLEQNDLEPGHTELLRE 65

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              ||  :|| |||:|:    :  |           | : : |:    :|:
Db         66 LLASLRRHDLLRRVDDFEAGAAAGAAPGEEDLCAAFNVICDNVGK 110


RESULT 5
A89822
RNA polymerase beta-prime chain [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A89822
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; H
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89822
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1207 <KUR>
A;Cross-references: UNIPROT:P60285; GB:BA000018; PID:g13700434; PIDN:BAB41732.1; GSPDB:GN
A;Experimental source: strain N315
C;Genetics:
A;Gene: rpoC
C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

  Query Match            14.9%;  Score 77.5;  DB 2;  Length 1207;
  Best Local Similarity   23.6%;  Pred. No. 24;
  Matches   26;  Conservative   21;  Mismatches   26;  Indels   37;  Gaps    4;

Qy          2 SRMSAEVIHQVEEALDTDEKEMLL--------------------------------FLC 28
              ::| || |  : | :| ||:  ||                                 ::
Db        168 AKMGAEGIKDLLEEIDLDEELKLLRDELESATGQRLTRAIKRLEVVESFRNSGNKPSWMI 227

Qy         29 RDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRV-RRFDLLKRILKM 77
               || : ::|| :| :: :  : |: :  || :|  ||  | : |||:| :
Db        228 LDV-LPIIPPEIRPMVQL--DGGRFATSDLNDLYRRVINRNNRLKRLLDL 274


RESULT 6
D90198
transposase ISC1234 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: D90198
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-W
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: D90198
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-312 <KUR>
A;Cross-references: UNIPROT:Q9UWT0; GB:AE006641; NID:g13813685; PIDN:AAK40843.1; GSPDB:GN
C;Genetics:
A;Gene: SSO0524
C;Superfamily: Sulfolobus solfataricus hypothetical protein c0626

  Query Match            14.8%;  Score 77;  DB 2;  Length 312;
  Best Local Similarity   28.7%;  Pred. No. 5.8;
  Matches   29;  Conservative   20;  Mismatches   32;  Indels   20;  Gaps    4;
```

```
Qy          11 QVEEALDTDEKE----------------MLLFLC--RDVAIDVVPPNVRDLLDILRERGK 52
               :::  ||| : |                |:|: |  || |: :|  ||     : |: ||
Db          31 EIKPVLDTMDLERVLGEGALVYLKLLVVMVLYSCSYRD-AVKMVNVNVVVAWFVGRKVGK 89

Qy          53 LSVGDLAELLYRVRRFDLLKRILKMDRKAVETHLLRNPHLV 93
                :: |    || ||:  ||:   |:: | : ::|  : |||
Db          90 STLHDFVGRLYGVRK-KLLEISFKLEEKCLPSYLPASAHLV 129


RESULT 7
D90350
transposase ISC1234 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: D90350
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: D90350
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KUR>
A;Cross-references: UNIPROT:Q97X83; GB:AE006641; NID:g13815125; PIDN:AAK42059.1; GSPDB:G
C;Genetics:
A;Gene: SSO1871
C;Superfamily: Sulfolobus solfataricus hypothetical protein c0626

  Query Match             14.8%;  Score 77;  DB 2;  Length 319;
  Best Local Similarity   28.7%;  Pred. No. 6;
  Matches   29;  Conservative   20;  Mismatches   32;  Indels   20;  Gaps    4;

Qy          11 QVEEALDTDEKE----------------MLLFLC--RDVAIDVVPPNVRDLLDILRERGK 52
               :::  ||| : |                |:|: |  || |: :|  ||     : |: ||
Db          38 EIKPVLDTMDLERVLGEGALVYLKLLIVMVLYSCSYRD-AVKMVNVNVVVAWFVGRKVGK 96

Qy          53 LSVGDLAELLYRVRRFDLLKRILKMDRKAVETHLLRNPHLV 93
                :: |    || ||:  ||:   |:: | : ::|  : |||
Db          97 STLHDFVGRLYGVRK-KLLEISFKLEEKCLPSYLPASAHLV 136


RESULT 8
E90466
transposase ISC1234 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: E90466; B90484
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: E90466
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KUR>
A;Cross-references: UNIPROT:Q97TU8; GB:AE006641; NID:g13816245; PIDN:AAK42988.1; GSPDB:G
A;Accession: B90484
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KU2>
A;Cross-references: GB:AE006641; NID:g13816422; PIDN:AAK43129.1; GSPDB:GN00155
C;Genetics:
A;Gene: SSO2882; SSO3028
C;Superfamily: Sulfolobus solfataricus hypothetical protein c0626

  Query Match             14.8%;  Score 77;  DB 2;  Length 319;
  Best Local Similarity   28.7%;  Pred. No. 6;
  Matches   29;  Conservative   20;  Mismatches   32;  Indels   20;  Gaps    4;

Qy          11 QVEEALDTDEKE----------------MLLFLC--RDVAIDVVPPNVRDLLDILRERGK 52
               :::  ||| : |                |:|: |  || |: :|  ||     : |: ||
Db          38 EIKPVLDTMDLERVLGEGALVYLKLLIVMVLYSCSYRD-AVKMVNVNVVVAWFVGRKVGK 96

Qy          53 LSVGDLAELLYRVRRFDLLKRILKMDRKAVETHLLRNPHLV 93
                :: |    || ||:  ||:   |:: | : ::|  : |||
Db          97 STLHDFVGRLYGVRK-KLLEISFKLEEKCLPSYLPASAHLV 136


RESULT 9
T05430
hypothetical protein F28A23.180 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05430
R;Bevan, M.; Weichselgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A.; Ne
submitted to the Protein Sequence Database, October 1998
A;Reference number: Z15415
A;Accession: T05430
A;Molecule type: DNA
A;Residues: 1-917 <BEV>
A;Cross-references: UNIPROT:O49498; EMBL:AL021961
A;Experimental source: cultivar Columbia; BAC clone F28A23
C;Genetics:
A;Map position: 4
A;Introns: 41/3; 70/3; 88/1; 118/1; 321/1; 367/1; 474/1; 504/2; 624/3; 655/2; 667/3; 695/
A;Note: F28A23.180
C;Superfamily: Arabidopsis thaliana hypothetical protein F28A23.180

  Query Match             14.8%;  Score 77;  DB 2;  Length 917;
  Best Local Similarity   23.8%;  Pred. No. 20;
  Matches   25;  Conservative   26;  Mismatches   48;  Indels    6;  Gaps    2;

Qy           2 SRMSAEVIHQVEEALD---TDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDL 58
               |: : :  : | | |:   | :|:  |    || : :    ::    :| ||       |:
Db         329 SKQTKKSANNVIEHLNRQITYQKDHGLSSLADVPLHIEDTLIKSASSVLSERPIKKTKDI 388

Qy          59 AELLYRVRRFDLLKRI---LKMDRKAVETHLLRNPHLVSDYRVLM 100
               |:|:  : |  : |::   :| |:| |   :  :|  : :: |||
Db         389 AKLIKDMGRLKINKKVTTMIKADKKLVTAKVNLDPETIKEWDVLM 433


RESULT 10
T10908
DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - Staphylococcus aureus (fragment)
C;Species: Staphylococcus aureus
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10908
R;Morse, R.; Collins, M.D.; Balsdon, J.T.; Reading, S.; Richardson, P.T.
submitted to the EMBL Data Library, June 1995
A;Description: Cloning part of the rpoC gene encoding the B' subunit of the DNA-dependent
A;Reference number: Z16792
A;Accession: T10908
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1057 <MOR>
A;Cross-references: UNIPROT:P47770; EMBL:X89233; NID:e984147; PID:e187583
A;Experimental source: strain NCDO949
C;Genetics:
A;Gene: rpoC
C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain
C;Keywords: nucleotidyltransferase; transcription

  Query Match             14.5%;  Score 75.5;  DB 2;  Length 1057;
  Best Local Similarity   23.6%;  Pred. No. 32;
  Matches   26;  Conservative   20;  Mismatches   27;  Indels   37;  Gaps    4;

Qy           2 SRMSAEVIHQVEEALDTDEKEMLL--------------------------------FLC 28
               ::| || |  : | :| ||:  ||                                 ::
Db         168 AKMGAEGIKDLLEEIDLDEELKLLRDELESATGQRLTRAIKRLEVVESFRNSGNKPSWMI 227

Qy          29 RDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRV-RRFDLLKRILKM 77
```

```
              || : ::|| :| :  :  : |: :  || :|  ||  | : |||:| :
Db        228 LDV-LPIIPPEIRPMAQL--DGGRFATSDLNDLYRRVINRNNRLKRLLDL 274
```

RESULT 11
B71724
dna-directed RNA polymerase beta prime chain (rpoC) RP141 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: B71724
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: B71724
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1372 <AND>
A;Cross-references: UNIPROT:Q9ZE20; GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA1460
A;Experimental source: strain Madrid E
C;Genetics:
A;Gene: rpoC; RP141
C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

  Query Match 14.5%; Score 75.5; DB 2; Length 1372;
  Best Local Similarity 28.9%; Pred. No. 44;
  Matches 26; Conservative 25; Mismatches 30; Indels 9; Gaps 6;

```
Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 60
              | :   : :  ||: |::: |   : :  || : |:|| :| |  :: : |: :  || |
Db        213 KKKKLVKRLKLVEDFLESENKPEWMIM--DV-LPVIPPEIRPL--VMLDGGRFATSDLNE 267

Qy         61 LLYRV-RRFDLLKRILKMDRKAVETHLLRN 89
              |  ||  | : ||:::  : || :  ::||
Db        268 LYRRVINRNNRLKKLI--ESKAPDI-IVRN 294
```

RESULT 12
G83112
DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain PA4269 [similarity] - Pseudomonas a
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G83112
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83112
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1399 <STO>
A;Cross-references: UNIPROT:Q9HWC9; GB:AE004842; GB:AE004091; NID:g9950481; PIDN:AAG0765
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: rpoC; PA4269
C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain
C;Keywords: nucleotidyltransferase

  Query Match 14.5%; Score 75.5; DB 2; Length 1399;
  Best Local Similarity 23.0%; Pred. No. 45;
  Matches 28; Conservative 25; Mismatches 30; Indels 39; Gaps 5;

```
Qy          2 SRMSAEVIHQVEEALD--------------TDEKEMLLFLCRDV---------------- 31
              :|| || :|::  |:|              |: :  :  | : :
Db        178 ARMGAEAVHELLNAIDLEHEIGRLREEIPQTNSETKIKKLSKRLKLMEAFQGSGNKPEWM 237

Qy         32 ---AIDVVPPNVRDLLDILRERGKLSVGDLAELLYRV-RRFDLLKRILKMDRKAVETHLL 87
                : |:||::| |: :  : |: :  || :|  ||  | : |||:| :   |    ::
Db        238 VLTVLPVLPPDLRPLVPL--DGGRFATSDLNDLYRRVINRNNRLKRLLDL---AAPDIIV 292

Qy         88 RN 89
```

```
              ||
Db        293 RN 294
```

RESULT 13
G82336
DNA-directed RNA polymerase, beta' chain VC0329 [imported] - Vibrio cholerae (strain N16
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82336
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: G82336
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1401 <HEI>
A;Cross-references: UNIPROT:Q9KV29; GB:AE004121; GB:AE003852; NID:g9654739; PIDN:AAF9350
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0329
A;Map position: 1
C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

  Query Match 14.4%; Score 75; DB 2; Length 1401;
  Best Local Similarity 23.4%; Pred. No. 50;
  Matches 33; Conservative 23; Mismatches 31; Indels 54; Gaps 7;

```
Qy          2 SRMSAEVI-------------HQVEEALDTDEKE-------------------------M 23
              ::| || |               |: | |||   |                         |
Db        178 AKMGAEAIKDLLASMDLPAEAEQMREELDTTNSETKRKKLTKRLKLVEAFVASGNKPEWM 237

Qy         24 LLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRV-RRFDLLKRILKMDRKAV 82
              :|       : |:||::| |: :  : |: :  || :|  ||  | : |||:|::   |
Db        238 IL-----TVLPVLPPDLRPLVPL--DGGRFATSDLNDLYRRVINRNNRLKRLLEL---AA 287

Qy         83 ETHLLRNPHLVSDYRVLMSEI 103
                ::||     : |:|   :
Db        288 PDIIVRN-----EKRMLQESV 303
```

RESULT 14
T37338
probable 35.9K protein - vaccinia virus (strain Ankara)
C;Species: vaccinia virus
A;Variety: strain Ankara
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 12-Jul-2004
C;Accession: T37338
R;Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
submitted to the EMBL Data Library, March 1997
A;Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strai
A;Reference number: Z20877
A;Accession: T37338
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-312 <ANT>
A;Cross-references: EMBL:U94848; PIDN:AAB96433.1
A;Experimental source: strain Ankara
C;Genetics:
A;Note: MVA062L
C;Superfamily: DNA-binding virion core protein, I1L type

  Query Match 14.1%; Score 73.5; DB 2; Length 312;
  Best Local Similarity 25.6%; Pred. No. 13;
  Matches 23; Conservative 26; Mismatches 30; Indels 11; Gaps 5;

```
Qy          7 EVIHQV--EEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYR 64
              ::|:|:  :|::  |||  :    :| :: |:|    :|:|:|: |   |      :: |
Db        158 DLINQLVKDESIQLDEKSSI----KD-SMYVIPD---ELIDVLKTRLFRSPQVKDNIISR 209
```

```
Qy          65 VRRFDLLKRILKMDRKAVETHLLRNPHLVS 94
               | :|    |: | |   ::    :|::| : |
Db         210 TRLYDYFTRVTKRDESSIYV-ILKDPRIAS 238
```

RESULT 15
PN0121
I1L protein - vaccinia virus (strains L-IVP and WR)
N;Alternate names: 36K protein
C;Species: vaccinia virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 12-Jul-2004
C;Accession: PN0121; A29889
R;Rjazankina, O.I.; Shchelkunov, S.N.; Muravlev, A.I.; Netesova, N.A.; Mikrjukov, N.N.;
Mol. Biol. (Mosk.) 24, 968-976, 1990
A;Title: The molecular biological study of vaccinia virus genome II; localization and fi
A;Reference number: PN0119; MUID:91066899; PMID:2250685
A;Accession: PN0121
A;Molecule type: DNA
A;Residues: 1-312 <RJA>
A;Experimental source: strain L-IVP
R;Schmitt, J.F.C.; Stunnenberg, H.G.
J. Virol. 62, 1889-1897, 1988
A;Title: Sequence and transcriptional analysis of the vaccinia virus HindIII I fragment.
A;Reference number: A29889; MUID:88215015; PMID:2835495
A;Accession: A29889
A;Molecule type: DNA
A;Residues: 1-20 <SCH>
A;Cross-references: GB:J03399; NID:g335662; PIDN:AAB59803.1; PID:g555408
A;Experimental source: strain WR
C;Genetics:
A;Gene: I1
C;Superfamily: DNA-binding virion core protein, I1L type
C;Keywords: glycoprotein; late protein
F;292,304/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match 14.1%; Score 73.5; DB 2; Length 312;
  Best Local Similarity 25.6%; Pred. No. 13;
  Matches 23; Conservative 26; Mismatches 30; Indels 11; Gaps 5;

```
Qy           7 EVIHQV--EEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYR 64
               ::|:|:  :|::  |||  :    :| :: |:|    :|:|:|: |   |      :: |
Db         158 DLINQLVKDESIQLDEKSSI----KD-SMYVIPD---ELIDVLKTRLFRSPQVKDNIISR 209

Qy          65 VRRFDLLKRILKMDRKAVETHLLRNPHLVS 94
               | :|    |: | |   ::    :|::| : |
Db         210 TRLYDYFTRVTKRDESSIYV-ILKDPRIAS 238
```

RESULT 16
E72157
L1L protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 12-Jul-2004
C;Accession: E72157
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar
submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A;Reference number: A72150
A;Accession: E72157
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-312 <SHC>
A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54655.1; PID:g5830616
A;Experimental source: strain Garcia-1966
C;Genetics:
A;Gene: L1L
C;Superfamily: DNA-binding virion core protein, I1L type

  Query Match 14.1%; Score 73.5; DB 2; Length 312;
  Best Local Similarity 25.6%; Pred. No. 13;
  Matches 23; Conservative 26; Mismatches 30; Indels 11; Gaps 5;

```
Qy           7 EVIHQV--EEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYR 64
               ::|:|:  :|::  |||  :    :| :: |:|    :|:|:|: |   |      :: |
Db         158 DLINQLVKDESIQLDEKSSI----KD-SMYVIPD---ELIDVLKTRLFRSPQVKDNIISR 209

Qy          65 VRRFDLLKRILKMDRKAVETHLLRNPHLVS 94
               | :|    |: | |   ::    :|::| : |
Db         210 TRLYDYFTRVTKRDESSIYV-ILKDPRIAS 238
```

RESULT 17
F42510
I1L protein - vaccinia virus (strain Copenhagen)
C;Species: vaccinia virus
A;Note: host Homo sapiens (man)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 12-Jul-2004
C;Accession: F42510
R;Johnson, G.P.
submitted to GenBank, June 1990
A;Reference number: A33172
A;Accession: F42510
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-312 <JOH>
A;Cross-references: UNIPROT:P20498
C;Superfamily: DNA-binding virion core protein, I1L type

  Query Match 14.1%; Score 73.5; DB 2; Length 312;
  Best Local Similarity 25.6%; Pred. No. 13;
  Matches 23; Conservative 26; Mismatches 30; Indels 11; Gaps 5;

```
Qy           7 EVIHQV--EEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYR 64
               ::|:|:  :|::  |||  :    :| :: |:|    :|:|:|: |   |      :: |
Db         158 DLINQLVKDESIQLDEKSSI----KD-SMYVIPD---ELIDVLKTRLFRSPQVKDNIISR 209

Qy          65 VRRFDLLKRILKMDRKAVETHLLRNPHLVS 94
               | :|    |: | |   ::    :|::| : |
Db         210 TRLYDYFTRVTKRDESSIYV-ILKDPRIAS 238
```

RESULT 18
S33070
I1L protein - variola virus
N;Alternate names: K1L protein
C;Species: variola virus
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 12-Jul-2004
C;Accession: S33070; H36842
R;Shchelkunov, S.N.; Blinov, V.M.; Totmenin, A.V.; Marennikova, S.S.; Kolykhalov, A.A.; I
dzhaparidze, O.G.; Sandakhchiev, L.S.
Virus Res. 27, 25-35, 1993
A;Title: Nucleotide sequence analysis of variola virus HindIII M, L, I genome fragments.
A;Reference number: S33069; MUID:93190624; PMID:8383392
A;Accession: S33070
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-312 <SHC>
A;Cross-references: UNIPROT:P32999; EMBL:X67119; NID:g62330; PIDN:CAA47555.1; PID:g62332
A;Experimental source: strain India-1967, isolate Ind3
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1992
R;Blinov, V.M.
submitted to GenBank, November 1992
A;Reference number: A36859
A;Accession: H36842
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-312 <BLI>
A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA48996.1; PID:g297236
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
C;Superfamily: DNA-binding virion core protein, I1L type

  Query Match 14.1%; Score 73.5; DB 2; Length 312;
  Best Local Similarity 24.0%; Pred. No. 13;
  Matches 24; Conservative 28; Mismatches 37; Indels 11; Gaps 5;

```
Qy           7 EVIHQV--EEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYR 64
```

```
              ::|:|:  :|::  |||  :    :| :: |:|    :|:|:|: |   |      ::
Db        158 DLINQLVKDESIQLDEKSSI----KD-SMYVIPD---ELIDVLKTRSFRSPQVKDNIISS 209

Qy         65 VRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIG 104
               | :|   |: | |  ::   :|::| : |   :   |:|
Db        210 TRLYDYFTRVTKRDESSIYV-ILKDPRIASILSLETVEMG 248


RESULT 19
T27903
hypothetical protein ZK546.14 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27903
R;Hallsworth, K.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid ZK546.
A;Reference number: Z20437
A;Accession: T27903
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-472 <HAL>
A;Cross-references: UNIPROT:Q23525; EMBL:U29380; PIDN:AAA68745.1; CESP:ZK546.14
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:ZK546.14
A;Introns: 18/3; 56/1; 342/3; 441/3

  Query Match             14.1%;  Score 73.5;  DB 2;  Length 472;
  Best Local Similarity   28.3%;  Pred. No. 20;
  Matches   30;  Conservative   19;  Mismatches   30;  Indels   27;  Gaps    5;

Qy          6 AEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRV 65
              || :  ||:|:|  ||||| |       :::| |     | ::|  |:
Db          2 AETLEAVEDAVDILEKEMLSF------CNLIPVNSWGFDDDVKESLKM------------ 43

Qy         66 RRFDLLKRIL-KMDRKAV----ETHLLRN----PHLVSDYRVLMSE 102
              |:  |: | | | :||::    : || :     |: | :    ||:
Db         44 RKHSLVNRQLSKKERKSMSAQQKQHLAKGLGLVPNTVQEVLEWMSK 89


RESULT 20
F97722
hypothetical protein rpoC [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97722
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: F97722
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1372 <KUR>
A;Cross-references: UNIPROT:Q9RH40; GB:AE006914; PIDN:AAL02720.1; PID:g15619230; GSPDB:G
C;Genetics:
A;Gene: rpoC
C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

  Query Match             14.1%;  Score 73.5;  DB 2;  Length 1372;
  Best Local Similarity   28.9%;  Pred. No. 68;
  Matches   26;  Conservative   24;  Mismatches   31;  Indels    9;  Gaps    6;

Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 60
              | :   : :  ||  |::: |   : :  || : |:|| :| |  :: : |: :  || |
Db        213 KKKKLVKRLKLVENFLESENKPEWMIM--DV-LPVIPPEIRPL--VMLDGGRFATSDLNE 267

Qy         61 LLYRV-RRFDLLKRILKMDRKAVETHLLRN 89
              |  ||  | : ||:::  : || :  ::||
Db        268 LYRRVINRNNRLKKLI--ESKAPDI-IVRN 294
```

```
RESULT 21
S41467
DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 20-May-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S41467; S41463; C72373
R;Palm, P.; Schleper, C.; Arnold-Ammer, I.; Holz, I.; Meier, T.; Lottspeich, F.; Zillig,
Nucleic Acids Res. 21, 4904-4908, 1993
A;Title: The DNA-dependent RNA-polymerase of Thermotoga maritima; characterisation of the
A;Reference number: S41462; MUID:94232816; PMID:8177738
A;Accession: S41467
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1690 <PAL>
A;Cross-references: UNIPROT:P36252; EMBL:X72695; NID:g425255; PIDN:CAA51247.1; PID:g42525
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993
A;Accession: S41463
A;Molecule type: protein
A;Residues: 2-3,'XX',6-20,'X',22-25,'X',27-28 <PAW>
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequ
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: C72373
A;Molecule type: DNA
A;Residues: 1-1690 <ARN>
A;Cross-references: GB:AE001724; GB:AE000512; NID:g4980966; PIDN:AAD35544.1; PID:g498096
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: rpoC
C;Complex: the enzyme consists of the sigma chain and the core enzyme; the sigma chain is
; the core enzyme is composed of two alpha chains, one beta chain, and one beta' chain
C;Function:
A;Description: the DNA-directed RNA polymerase, also called transcriptase, catalyzes RNA
C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain
C;Keywords: nucleotidyltransferase; transcription

  Query Match             14.1%;  Score 73.5;  DB 2;  Length 1690;
  Best Local Similarity   28.0%;  Pred. No. 86;
  Matches   23;  Conservative   21;  Mismatches   29;  Indels    9;  Gaps    4;

Qy          9 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYR-VRR 67
              :  |:: | :  |   : |     : |:||::| :: |  | |: :  || ||  | : |
Db        505 LKMVKDFLKSGNKPEWMVL---EVVPVIPPDLRPMIQI--EGGRFATTDLNELYRRLINR 559

Qy         68 FDLLKRILKMDRKAVETHLLRN 89
              : ||::|::    :   :|||
Db        560 NNRLKKLLELGAPEI---ILRN 578


RESULT 22
D90344
transposase ISC1234 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: D90344
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Y
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: D90344
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KUR>
A;Cross-references: UNIPROT:Q97XD0; GB:AE006641; NID:g13815069; PIDN:AAK42011.1; GSPDB:GN
C;Genetics:
A;Gene: SSO1814
C;Superfamily: Sulfolobus solfataricus hypothetical protein c0626
```

```
  Query Match             14.0%;  Score 73;  DB 2;  Length 319;
  Best Local Similarity   34.2%;  Pred. No. 14;
  Matches   25;  Conservative   16;  Mismatches   28;  Indels    4;  Gaps    3;

Qy         23 MLLFLC--RDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRILKMDRK 80
              |:|: |  || |: :|  ||     : |: || :: |    || ||:  ||:   |:: |
Db         66 MVLYSCSYRD-AVKMVNVNVVVAWFVGRKVGKSTLHDFVGRLYGVRK-KLLEISFKLEEK 123

Qy         81 AVETHLLRNPHLV 93
                : ::|  : |||
Db        124 CLPSYLPASAHLV 136


RESULT 23
D90342
transposase ISC1234 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: D90342
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: D90342
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KUR>
A;Cross-references: UNIPROT:Q97XE6; GB:AE006641; NID:g13815051; PIDN:AAK41995.1; GSPDB:G
C;Genetics:
A;Gene: SSO1801
C;Superfamily: Sulfolobus solfataricus hypothetical protein c0626

  Query Match             14.0%;  Score 73;  DB 2;  Length 319;
  Best Local Similarity   34.2%;  Pred. No. 14;
  Matches   25;  Conservative   16;  Mismatches   28;  Indels    4;  Gaps    3;

Qy         23 MLLFLC--RDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRILKMDRK 80
              |:|: |  || |: :|  ||     : |: || :: |    || ||:  ||:   |:: |
Db         66 MVLYSCSYRD-AVKMVNVNVVVAWFVGRKVGKSTLHDFVGRLYGVRK-KLLEISFKLEEK 123

Qy         81 AVETHLLRNPHLV 93
                : ::|  : |||
Db        124 CLPSYLPASAHLV 136


RESULT 24
S74012
hypothetical protein c0626 - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S74012
R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.
Mol. Microbiol. 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal genome: 1
A;Reference number: S73076; MUID:97055432; PMID:8899719
A;Accession: S74012
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-319 <SEN>
A;Cross-references: UNIPROT:P95873; EMBL:Y08256; NID:g1707679; PID:g1707705
A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C;Superfamily: Sulfolobus solfataricus hypothetical protein c0626

  Query Match             14.0%;  Score 73;  DB 2;  Length 319;
  Best Local Similarity   34.2%;  Pred. No. 14;
  Matches   25;  Conservative   16;  Mismatches   28;  Indels    4;  Gaps    3;

Qy         23 MLLFLC--RDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRILKMDRK 80
              |:|: |  || |: :|  ||     : |: || :: |    || ||:  ||:   |:: |
Db         66 MVLYSCSYRD-AVKMVNVNVVVAWFVGRKVGKSTLHDFVGRLYGVRK-KLLEISFKLEEK 123

Qy         81 AVETHLLRNPHLV 93
                : ::|  : |||
Db        124 CLPSYLPASAHLV 136


RESULT 25
H90321
transposase ISC1234 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H90321; F90429; C90306; G90299; D90294; D90352
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H90321
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KUR>
A;Cross-references: UNIPROT:Q97TU6; GB:AE006641; NID:g13814857; PIDN:AAK41831.1; GSPDB:GN
A;Accession: F90429
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KU2>
A;Cross-references: GB:AE006641; NID:g13815869; PIDN:AAK42693.1; GSPDB:GN00155
A;Accession: C90306
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KU3>
A;Cross-references: GB:AE006641; NID:g13814708; PIDN:AAK41706.1; GSPDB:GN00155
A;Accession: G90299
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KU4>
A;Cross-references: GB:AE006641; NID:g13814644; PIDN:AAK41654.1; GSPDB:GN00155
A;Accession: D90294
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KU5>
A;Cross-references: GB:AE006641; NID:g13814591; PIDN:AAK41611.1; GSPDB:GN00155
A;Accession: D90352
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KU6>
A;Cross-references: GB:AE006641; NID:g13815143; PIDN:AAK42075.1; GSPDB:GN00155
C;Genetics:
A;Gene: SSO1616; SSO2567; SSO1481; SSO1420; SSO1377; SSO1883
C;Superfamily: Sulfolobus solfataricus hypothetical protein c0626

  Query Match             14.0%;  Score 73;  DB 2;  Length 319;
  Best Local Similarity   34.2%;  Pred. No. 14;
  Matches   25;  Conservative   16;  Mismatches   28;  Indels    4;  Gaps    3;

Qy         23 MLLFLC--RDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRILKMDRK 80
              |:|: |  || |: :|  ||     : |: || :: |    || ||:  ||:   |:: |
Db         66 MVLYSCSYRD-AVKMVNVNVVVAWFVGRKVGKSTLHDFVGRLYGVRK-KLLEISFKLEEK 123

Qy         81 AVETHLLRNPHLV 93
                : ::|  : |||
Db        124 CLPSYLPASAHLV 136


RESULT 26
G90428
transposase ISC1234 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: G90428
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
```

```
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90428
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KUR>
A;Cross-references: UNIPROT:Q97VQ6; GB:AE006641; NID:g13815862; PIDN:AAK42686.1; GSPDB:G
C;Genetics:
A;Gene: SSO2557
C;Superfamily: Sulfolobus solfataricus hypothetical protein c0626

  Query Match             14.0%;  Score 73;  DB 2;  Length 319;
  Best Local Similarity   34.2%;  Pred. No. 14;
  Matches   25;  Conservative   16;  Mismatches   28;  Indels    4;  Gaps    3;

Qy         23 MLLFLC--RDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRILKMDRK 80
              |:|: |  || |: :|  ||     : |: || :: |    || ||:  ||:   |:: |
Db         66 MVLYSCSYRD-AVKMVNVNVVVAWFVGRKVGKSTLHDFVGRLYGVRK-KLLEISFKLEEK 123

Qy         81 AVETHLLRNPHLV 93
                : ::|  : |||
Db        124 CLPSYLPASAHLV 136


RESULT 27
T00344
hypothetical protein KIAA0586 - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00344
R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
DNA Res. 5, 31-39, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complet
A;Reference number: Z14086; MUID:98290545; PMID:9628581
A;Accession: T00344
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1533 <NAG>
A;Cross-references: UNIPROT:Q9BVV6; EMBL:AB011158; NID:g3043695; PIDN:BAA25512.1; PID:g3
A;Experimental source: brain
C;Genetics:
A;Note: KIAA0586

  Query Match             14.0%;  Score 73;  DB 2;  Length 1533;
  Best Local Similarity   28.8%;  Pred. No. 85;
  Matches   21;  Conservative   12;  Mismatches   28;  Indels   12;  Gaps    2;

Qy         29 RDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRILKMDR------KAV 82
              :|||: |:|      || : |  |    |:    | : : | |: :||        | |
Db         79 KDVAVQVLP------LDKIEENNKQKANDIFISQYTMGQKDALRTVLKQKAQSMPVFKEV 132

Qy         83 ETHLLRNPHLVSD 95
              : ||| :  :  |
Db        133 KVHLLEDAGIEKD 145


RESULT 28
I48157
protein kinase (EC 2.7.1.37) cdk2L - golden hamster
N;Contains: protein kinase cdk2
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I48157; I48156
R;Noguchi, E.; Sekiguchi, T.; Yamashita, K.; Nishimoto, T.
Biochem. Biophys. Res. Commun. 197, 1524-1529, 1993
A;Title: Molecular cloning and identification of two types of hamster cyclin-dependent k
A;Reference number: I48156; MUID:94107363; PMID:8280171
A;Accession: I48157
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-346 <RES>
A;Cross-references: UNIPROT:Q60545; GB:D17351; NID:g464160; PIDN:BAA04166.1; PID:g666952
A;Accession: I48156
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-196,245-346 <RE2>
A;Cross-references: GB:D17350; NID:g464159; PIDN:BAA04165.1; PID:g666951
C;Complex: In various organisms, cdc2 has been identified as a component of the M-phase
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; cell cycle control; phosphotransferase; serine/threonine-specific protei
F;1-196,245-346/Product: protein kinase cdc2 #status predicted <MAT2>
F;2-303/Domain: protein kinase homology #status atypical <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

  Query Match             13.9%;  Score 72.5;  DB 1;  Length 346;
  Best Local Similarity   29.1%;  Pred. No. 18;
  Matches   25;  Conservative   20;  Mismatches   26;  Indels   15;  Gaps    4;

Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAI--DVVPPNVRDLLDILRERGKLSVGDL 58
              |:::: ||:   :  |||: : :     |::::  ::  ||:  |||::    |
Db         22 KNKLTGEVVALKKIRLDTETEGVPSTAIREISLLKELNHPNIVKLLDVIHTENK------ 75

Qy         59 AELLYRVRRFDLLKRILK--MDRKAV 82
                || |  |:|| : ||  ||  ||
Db         76 ---LYLV--FELLHQDLKKFMDASAV 96


RESULT 29
B84448
hypothetical protein At2g03410 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84448
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84448
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <STO>
A;Cross-references: UNIPROT:Q9ZQ77; GB:AE002093; NID:g4335758; PIDN:AAD17435.1; GSPDB:GN
C;Genetics:
A;Gene: At2g03410
A;Map position: 2
C;Superfamily: Saccharomyces hypothetical protein YKL189w

  Query Match             13.9%;  Score 72.5;  DB 2;  Length 348;
  Best Local Similarity   25.2%;  Pred. No. 18;
  Matches   34;  Conservative   20;  Mismatches   38;  Indels   43;  Gaps    5;

Qy          1 KSRMSAEVIHQVEEAL---DTDEKE----------MLLFLCRDVAIDVVPPNVRDLLDIL 47
              |||:  |:: |  : :   :::|:|          :   |||         |:|||  ||
Db          8 KSRLPGEIVRQTRDLIALAESEEEETDARNSKRLGICAELCR---------NIRDLKSIL 58

Qy         48 RERGKLSVGDLAELLYRVRRF------DLLKRILKMDRKA--------------VETHL 86
                |:       | ||      |        |:| | |:| :|              ||  |
Db         59 YGNGEAEPVPEACLLLTQEFFRADTLRPLIKSIPKLDLEARKDATQIVANLQKQQVEFRL 118

Qy         87 LRNPHLVSDYRVLMS 101
              : : :| |:  |: |
Db        119 VASEYLESNLDVIDS 133


RESULT 30
JC4998
IMP dehydrogenase (EC 1.1.1.205) - Pyrococcus furiosus
C;Species: Pyrococcus furiosus
C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 09-Jul-2004
C;Accession: JC4998
R;Collart, F.R.; Osipiuk, J.; Trent, J.; Olsen, G.J.; Huberman, E.
```

Gene 174, 209-216, 1996
A;Title: Cloning, characterization and sequence comparison of the gene coding for IMP de
A;Reference number: JC4998; MUID:97045814; PMID:8890736
A;Accession: JC4998
A;Molecule type: DNA
A;Residues: 1-485 <COL>
A;Cross-references: UNIPROT:P42851; GB:U08814; NID:g595286; PIDN:AAC44532.1; PID:g595287
C;Genetics:
A;Gene: guaB
C;Complex: homotetramer
C;Function:
A;Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule c
A;Pathway: purine nucleotide biosynthesis
C;Superfamily: inosine-5'-monophosphate dehydrogenase; CBS homology; IMP dehydrogenase a
C;Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosyn
F;15-81/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F;102-149/Domain: CBS homology <CBS1>
F;159-207/Domain: CBS homology <CBS2>
F;208-447/Domain: IMP dehydrogenase catalytic homology <IDHC>
F;301/Active site: Cys #status predicted

Query Match 13.9%; Score 72.5; DB 1; Length 485;
Best Local Similarity 27.9%; Pred. No. 26;
Matches 31; Conservative 18; Mismatches 29; Indels 33; Gaps 6;

```
Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKL----SVG 56
              |  |: |||  | |::| :|          |: ::  |  | | :: | |||    ::
Db        153 KELMTREVI-TVPESVDVEE----------ALKIMMENRIDRLPVVNEDGKLVGLITMS 200

Qy         57 DL--------------AELLY--RVRRFDLLKRILKMDRKAVETHLLRNPH 91
              ||               |||    |  || |:| :::||  |:  ::   |
Db        201 DLVARKKYKNAVRNEKGELLVAAAVSPFD-LRRAIELDRAGVDVIVVDTAH 250
```

Search completed: September 30, 2005, 08:00:51
Job time : 41 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 30, 2005, 07:58:49 ; Search time 58 Seconds
(without alignments)
927.040 Million cell updates/sec

Title: US-09-402-569-2
Perfect score: 521
Sequence: 1 KSRMSAEVIHQVEEALDTDE.....LLRNPHLVSDYRVLMSEIGE 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	504	96.7	480	1	CFLA_HUMAN	O15519 h casp8 and
2	437	83.9	219	2	Q6QN98	Q6qn98 sus scrofa
3	437	83.9	487	2	Q6QN97	Q6qn97 sus scrofa
4	399	76.6	218	2	Q99MZ5	Q99mz5 rattus norv
5	390	74.9	481	2	Q812G4	Q812g4 mus musculu
6	390	74.9	484	1	CFLA_MOUSE	O35732 m casp8 and
7	154.5	29.7	497	2	Q6NTR7	Q6ntr7 xenopus lae
8	148	28.4	418	2	Q8UVG5	Q8uvg5 brachydanio
9	129.5	24.9	188	2	P88961	P88961 human herpe
10	121.5	23.3	241	1	CFLA_MCV1	Q98325 molluscum c
11	120	23.0	476	2	Q66II9	Q66ii9 brachydanio
12	120	23.0	476	2	Q9I8J3	Q9i8j3 brachydanio
13	119	22.8	369	2	O11300	O11300 molluscum c
14	119	22.8	371	2	Q98326	Q98326 molluscum c
15	115.5	22.2	482	2	Q90WU1	Q90wu1 gallus gall
16	114.5	22.0	480	1	ICE8_MOUSE	O89110 mus musculu
17	106.5	20.4	482	2	Q9JHX4	Q9jhx4 rattus norv
18	104.5	20.1	182	2	Q99CX0	Q99cx0 bovine herp
19	104.5	20.1	500	2	Q9IB64	Q9ib64 xenopus lae
20	99.5	19.1	171	1	CFLA_EHV2	Q66674 equine herp
21	98.5	18.9	278	2	Q6NVI2	Q6nvi2 homo sapien
22	98.5	18.9	479	1	ICE8_HUMAN	Q14790 h caspase-8
23	93	17.9	512	2	Q6PAD9	Q6pad9 xenopus lae
24	83	15.9	208	1	FADD_HUMAN	Q13158 homo sapien
25	81	15.5	1388	2	Q6MDM0	Q6mdm0 parachlamyd
26	79	15.2	247	2	Q68HC0	Q68hc0 homo sapien
27	79	15.2	455	2	Q6KF63	Q6kf63 homo sapien
28	79	15.2	478	2	Q6KF62	Q6kf62 homo sapien
29	79	15.2	521	1	ICEA_HUMAN	Q92851 homo sapien
30	79	15.2	522	2	Q8IUP5	Q8iup5 homo sapien
31	79	15.2	730	2	Q86M65	Q86m65 trypanosoma
32	79	15.2	1326	2	Q6Q8Z3	Q6q8z3 uncultured
33	79	15.2	1349	2	Q6AP77	Q6ap77 desulfotale
34	79	15.2	1513	2	Q72HM6	Q72hm6 thermus the
35	79	15.2	1524	1	RPOC_THETH	Q8rqe8 thermus the
36	78.5	15.1	131	1	YSO1_PLEBO	P51586 plectonema
37	78.5	15.1	997	2	Q7ZXX2	Q7zxx2 xenopus lae
38	78.5	15.1	1217	1	RPOC_ENTFA	Q82z41 enterococcu
39	78	15.0	95	2	Q6LCG1	Q6lcg1 homo sapien
40	78	15.0	772	2	P94866	P94866 leuconostoc
41	77.5	14.9	541	2	P95688	P95688 staphylococ
42	77.5	14.9	1199	2	Q65PB4	Q65pb4 bacillus li
43	77.5	14.9	1207	1	RPOC_STAAM	P60284 staphylococ
44	77.5	14.9	1207	1	RPOC_STAAN	P60285 staphylococ
45	77.5	14.9	1207	1	RPOC_STAAW	P60286 staphylococ

ALIGNMENTS

RESULT 1
CFLA_HUMAN
ID CFLA_HUMAN STANDARD; PRT; 480 AA.
AC O15519; O14673; O14674; O14675; O15137; O15138; O15356; O15510;
AC O43618; O43619; O43620; O60458; O60459; Q96TE4; Q9UEW1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE CASP8 and FADD-like apoptosis regulator precursor (Cellular FLICE-like
DE inhibitory protein) (c-FLIP) (Caspase-eight-related protein) (Casper)
DE (Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related
DE inducer of toxicity) (MRIT) (Caspase homolog) (CASH) (Inhibitor of
DE FLICE) (I-FLICE) (FADD-like antiapoptotic molecule 1) (Flame-1)
DE (Usurpin).
GN Name=CFLAR; Synonyms=CASH, CLARP, MRIT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 13 AND 14), AND MUTAGENESIS OF
RP TYR-360.
RC TISSUE=Embryonic kidney, and Umbilical vein endothelial cells;
RX MEDLINE=97352452; PubMed=9208847; DOI=10.1016/S1074-7613(00)80450-1;
RA Shu H.-B., Halpin D.R., Goeddel D.V.;
RT "Casper is a FADD- and caspase-related inducer of apoptosis.";
RL Immunity 6:751-763(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=97470967; PubMed=9326610; DOI=10.1073/pnas.94.21.11333;
RA Han D.K.M., Chaudhary P.M., Wright M.E., Friedman C., Trask B.J.,
RA Riedel R.T., Baskin D.G., Schwartz S.M., Hood L.;
RT "MRIT, a novel death-effector domain-containing protein, interacts
RT with caspases and BclXL and initiates cell death.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11333-11338(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=97360133; PubMed=9217161; DOI=10.1038/40657;
RA Irmler M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V.,
RA Bodmer J.-L., Schroeter M., Burns K., Mattmann C., Rimoldi D.,
RA French L.E., Tschopp J.;
RT "Inhibition of death receptor signals by cellular FLIP.";
RL Nature 388:190-195(1997).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 8; 9 AND 10), AND MUTAGENESIS OF
RP ASP-376.
RC TISSUE=T-cell;
RX MEDLINE=97373543; PubMed=9228018; DOI=10.1074/jbc.272.30.18542;
RA Srinivasula S.M., Ahmad M., Ottilie S., Bullrich F., Banks S.,
RA Wang Y., Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
RA Armstrong R.C., Alnemri E.S.;
RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
RT Fas/TNFR1-induced apoptosis.";

```
RL   J. Biol. Chem. 272:18542-18545(1997).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Umbilical vein endothelial cells;
RX   MEDLINE=97362203; PubMed=9211860; DOI=10.1074/jbc.272.28.17255;
RA   Hu S., Vincenz C., Ni J., Gentz R., Dixit V.M.;
RT   "I-FLICE, a novel inhibitor of tumor necrosis factor receptor-1- and
RT   CD-95-induced apoptosis.";
RL   J. Biol. Chem. 272:17255-17257(1997).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 7).
RA   Hu S., Dixit V.M.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 11 AND 12).
RC   TISSUE=Kidney;
RX   MEDLINE=99218584; PubMed=10200473;
RA   Rasper D.M., Vaillancourt J.P., Hadano S., Houtzager V.M., Seiden I.,
RA   Keen S.L.C., Tawa P., Xanthoudakis S., Nasir J., Martindale D.,
RA   Koop B.F., Peterson E.P., Thornberry N.A., Huang J., MacPherson D.P.,
RA   Black S.C., Hornung F., Lenardo M.J., Hayden M.R., Roy S.,
RA   Nicholson D.W.;
RT   "Cell death attenuation by 'Usurpin', a mammalian DED-caspase
RT   homologue that precludes caspase-8 recruitment and activation by the
RT   CD-95 (Fas, APO-1) receptor complex.";
RL   Cell Death Differ. 5:271-288(1998).
RN   [8]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   TISSUE=Skin fibroblast;
RX   MEDLINE=97426025; PubMed=9289491; DOI=10.1074/jbc.272.32.19641;
RA   Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
RA   Brodianskii V.M., Wallach D.;
RT   "CASH, a novel caspase homologue with death effector domains.";
RL   J. Biol. Chem. 272:19641-19644(1997).
RN   [9]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   TISSUE=Colon carcinoma;
RX   MEDLINE=98021435; PubMed=9380701; DOI=10.1073/pnas.94.20.10717;
RA   Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
RT   "CLARP, a death effector domain-containing protein interacts with
RT   caspase-8 and regulates apoptosis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
RN   [10]
RP   SEQUENCE FROM N.A. (ISOFORM 11).
RX   MEDLINE=21100893; PubMed=11161814; DOI=10.1006/geno.2000.6392;
RA   Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
RA   Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA   Ikeda J.-E., Hayden M.R.;
RT   "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
RT   and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RT   critical region at chromosome 2q33-q34: candidate genes for ALS2.";
RL   Genomics 71:200-213(2001).
RN   [11]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [12]
RP   FUNCTION.
RX   MEDLINE=99098897; PubMed=9889531;
RA   Scaffidi C., Schmitz I., Krammer P.H., Peter M.E.;
RT   "The role of c-FLIP in modulation of CD95-induced apoptosis.";
RL   J. Biol. Chem. 274:1541-1548(1999).
RN   [13]
RP   INDUCTION.
RX   MEDLINE=99244884; PubMed=10227994;
RA   Algeciras-Schimnich A., Griffith T.S., Lynch D.H., Paya C.V.;
RT   "Cell cycle-dependent regulation of FLIP levels and susceptibility to
RT   Fas-mediated apoptosis.";
RL   J. Immunol. 162:5205-5211(1999).
RN   [14]
RP   SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX   PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA   Hillman R.T., Green R.E., Brenner S.E.;
RT   "An unappreciated role for RNA surveillance.";
RL   Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
CC   -!- FUNCTION: Apoptosis regulator protein which may function as a
CC       crucial link between cell survival and cell death pathways in
CC       mammalian cells. Acts as an inhibitor of TNFRSF6 mediated
CC       apoptosis. A proteolytic fragment (p43) is likely retained in the
CC       death-inducing signaling complex (DISC) thereby blocking further
CC       recruitment and processing of caspase-8 at the complex. Full
CC       length and shorter isoforms have been shown either to induce
CC       apoptosis or to reduce TNFRSF-triggered apoptosis. Lacks enzymatic
CC       (caspase) activity.
CC   -!- SUBUNIT: TNFRSF6 stimulation triggers recruitment to the death-
CC       inducing signaling complex (DISC) formed by TNFRSF6, FADD and
CC       caspase-8. A proteolytic fragment (p43) stays associated with the
CC       DISC. Also interacts with caspase-10, caspase-3, TRAF1, TRAF2 and
CC       Bcl-X(L) (in vitro).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=14;
CC       Name=1; Synonyms=FLIP-L, CLARP1, MRIT alpha-1, CASH alpha, I-FLICE
CC       1, FLAME-1 gamma, Usurpin alpha;
CC         IsoId=O15519-1; Sequence=Displayed;
CC       Name=2; Synonyms=FLIP-S, CLARP2, MRIT beta-1, CASH beta;
CC         IsoId=O15519-2; Sequence=VSP_000828, VSP_000829;
CC       Name=3; Synonyms=MRIT alpha-2;
CC         IsoId=O15519-3; Sequence=VSP_000824, VSP_000838;
CC       Name=4; Synonyms=I-FLICE 2;
CC         IsoId=O15519-4; Sequence=VSP_000825;
CC       Name=5; Synonyms=I-FLICE 3;
CC         IsoId=O15519-5; Sequence=VSP_000840;
CC       Name=6; Synonyms=I-FLICE 4;
CC         IsoId=O15519-6; Sequence=VSP_000826, VSP_000841;
CC       Name=7; Synonyms=I-FLICE 5;
CC         IsoId=O15519-7; Sequence=VSP_000824, VSP_000827, VSP_000838;
CC       Name=8; Synonyms=Flame-1 alpha;
CC         IsoId=O15519-8; Sequence=VSP_000830;
CC       Name=9; Synonyms=Flame-1 beta;
CC         IsoId=O15519-9; Sequence=VSP_000830, VSP_000836, VSP_000837;
CC         Note=May be produced at very low levels due to a premature stop
CC         codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC       Name=10; Synonyms=Flame-1 delta;
CC         IsoId=O15519-10; Sequence=VSP_000834, VSP_000835;
CC       Name=11; Synonyms=Usurpin beta;
CC         IsoId=O15519-11; Sequence=VSP_000838;
CC       Name=12; Synonyms=Usurpin gamma;
CC         IsoId=O15519-12; Sequence=VSP_000832, VSP_000833;
CC       Name=13;
CC         IsoId=O15519-13; Sequence=VSP_000831;
CC       Name=14;
CC         IsoId=O15519-14; Sequence=VSP_000839;
CC   -!- TISSUE SPECIFICITY: Widely expressed. Higher expression in
CC       skeletal muscle, pancreas, heart, kidney, placenta, and peripheral
CC       blood leukocytes. Also detected in diverse cell lines. Isoform 8
CC       is predominantly expressed in testis and skeletal muscle.
```

```
CC   -!- INDUCTION: Repressed by IL-2 after TCR stimulation, during
CC       progression to the S-phase of the cell cycle.

  Query Match             96.7%;  Score 504;  DB 1;  Length 480;
  Best Local Similarity   99.0%;  Pred. No. 5.8e-39;
  Matches  101;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLY 60

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||||||||||||||||||||||||:||||
Db         61 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102


RESULT 2
Q6QN98
ID   Q6QN98      PRELIMINARY;      PRT;   219 AA.
AC   Q6QN98;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cellular FLICE-like inhibitory protein short form.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Goto Y., Maeda A., Matsuda F., Inoue N., Manabe N.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY533020; AAS22336.1; -.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   Pfam; PF01335; DED; 2.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS50168; DED; 2.
SQ   SEQUENCE   219 AA;  25303 MW;  840DC7135D88AAC8 CRC64;

  Query Match             83.9%;  Score 437;  DB 2;  Length 219;
  Best Local Similarity   85.4%;  Pred. No. 4.7e-33;
  Matches   88;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          3 RMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELL 62
              |||||||||||||| |||:|||||||:| |||| ||||||||||||||:  |||||
Db          5 RMSAEVIHQVEEALDEDEKEILLFLCRDIAADVVPLNVRDLLDILRERGKLSLVSLAELL 64

Qy         63 YRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||: ||  |||:|||:||||||| ||||
Db         65 YRVRRFDLLKRILKMDRRTVEAQLLRHPHLISDYRVLMMEIGE 107


RESULT 3
Q6QN97
ID   Q6QN97      PRELIMINARY;      PRT;   487 AA.
AC   Q6QN97;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cellular FLICE-like inhibitory protein long form.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Goto Y., Maeda A., Matsuda F., Inoue N., Manabe N.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY533021; AAS22337.1; -.
DR   HSSP; P55211; 1JXQ.
DR   GO; GO:0030693; F:caspase activity; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR001309; ICE_p20.
DR   InterPro; IPR002398; Peptidase_C14.
DR   Pfam; PF01335; DED; 2.
DR   SMART; SM00115; CASc; 1.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
SQ   SEQUENCE   487 AA;  56000 MW;  067BE3618EE9C0E7 CRC64;

  Query Match             83.9%;  Score 437;  DB 2;  Length 487;
  Best Local Similarity   85.4%;  Pred. No. 1.1e-32;
  Matches   88;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          3 RMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELL 62
              |||||||||||||| |||:|||||||:| |||| ||||||||||||||:  |||||
Db          5 RMSAEVIHQVEEALDEDEKEILLFLCRDIAADVVPLNVRDLLDILRERGKLSLVSLAELL 64

Qy         63 YRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||: ||  |||:|||:||||||| ||||
Db         65 YRVRRFDLLKRILKMDRRTVEAQLLRHPHLISDYRVLMMEIGE 107


RESULT 4
Q99MZ5
ID   Q99MZ5      PRELIMINARY;      PRT;   218 AA.
AC   Q99MZ5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   FLIP short form.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=22131045; PubMed=12135878;
RA   Xiao C.W., Asselin E., Tsang B.K.;
RT   "Nuclear factor kappaB-mediated induction of Flice-like inhibitory
RT   protein prevents tumor necrosis factor alpha-induced apoptosis in rat
RT   granulosa cells.";
RL   Biol. Reprod. 67:436-441(2002).
DR   EMBL; AF244366; AAK28358.1; -.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   Pfam; PF01335; DED; 2.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS50168; DED; 2.
SQ   SEQUENCE   218 AA;  24718 MW;  9DA9EBAF3441967B CRC64;

  Query Match             76.6%;  Score 399;  DB 2;  Length 218;
  Best Local Similarity   76.9%;  Pred. No. 1.7e-29;
  Matches   80;  Conservative    9;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          2 SRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAEL 61
              | :||||||||||:|| |||||:|||||||  :: ||||||||| | |||:||   ||||
Db          4 STVSAEVIHQVEESLDEDEKEMMLFLCRDVTENLAPPNVRDLLDCLSERGQLSFAALAEL 63

Qy         62 LYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||| |: ||| || |:||||||||||: ||||
Db         64 LYRVRRFDLLKRILKTDKAAVEDHLCRSPHLVSDYRVLLMEIGE 107


RESULT 5
```

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Q812G4
ID   Q812G4      PRELIMINARY;      PRT;   481 AA.
AC   Q812G4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CASP8 and FADD-like apoptosis regulator, isoform 1.
GN   Name=Cflar;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC029223; AAH29223.1; -.
DR   HSSP; Q9C0K4; 1QTN.
DR   MGD; MGI:1336166; Cflar.
DR   GO; GO:0030693; F:caspase activity; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR001309; ICE_p20.
DR   InterPro; IPR002398; Peptidase_C14.
DR   Pfam; PF01335; DED; 2.
DR   SMART; SM00115; CASc; 1.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
SQ   SEQUENCE   481 AA;  54874 MW;  433E07E2E5FA5A05 CRC64;

  Query Match             74.9%;  Score 390;  DB 2;  Length 481;
  Best Local Similarity   75.2%;  Pred. No. 2.8e-28;
  Matches   79;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 60
              :| :|||||||||| || |||||:|||||||  ::  |||||||| | |||:||   |||
Db          3 QSPVSAEVIHQVEECLDEDEKEMMLFLCRDVTENLAAPNVRDLLDSLSERGQLSFATLAE 62

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||| |:  || || ||||||||||||: ||||
Db         63 LLYRVRRFDLLKRILKTDKATVEDHLRRNPHLVSDYRVLLMEIGE 107


RESULT 6
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CFLA_MOUSE
ID   CFLA_MOUSE     STANDARD;      PRT;   484 AA.
AC   O35732; O35707; O35733;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   CASP8 and FADD-like apoptosis regulator precursor (Cellular FLICE-like
DE   inhibitory protein) (c-FLIP) (Caspase-eight-related protein) (Casper)
DE   (Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related
DE   inducer of toxicity) (MRIT) (Caspase homolog) (CASH) (Inhibitor of
DE   FLICE) (I-FLICE) (FADD-like antiapoptotic molecule 1) (Flame-1)
DE   (Usurpin).
GN   Name=Cflar; Synonyms=Cash;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   TISSUE=Liver;
RX   MEDLINE=97426025; PubMed=9289491; DOI=10.1074/jbc.272.32.19641;
RA   Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
RA   Brodianskii V.M., Wallach D.;
RT   "CASH, a novel caspase homologue with death effector domains.";
RL   J. Biol. Chem. 272:19641-19644(1997).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Heart;
RX   MEDLINE=97360133; PubMed=9217161; DOI=10.1038/40657;
RA   Irmler M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V.,
RA   Bodmer J.-L., Schroeter M., Burns K., Mattmann C., Rimoldi D.,
RA   French L.E., Tschopp J.;
RT   "Inhibition of death receptor signals by cellular FLIP.";
RL   Nature 388:190-195(1997).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=20350661; PubMed=10894163; DOI=10.1016/S1074-7613(00)80214-9;
RA   Yeh W.-C., Itie A., Elia A.J., Ng M., Shu H.-B., Wakeham A.,
RA   Mirtsos C., Suzuki N., Bonnard M., Goeddel D.V., Mak T.W.;
RT   "Requirement for Casper (c-FLIP) in regulation of death receptor-
RT   induced apoptosis and embryonic development.";
RL   Immunity 12:633-642(2000).
RN   [4]
RP   FUNCTION.
RX   MEDLINE=20069388; PubMed=10602037;
RX   DOI=10.1002/1521-4141(200001)30:1<155::AID-IMMU155>3.3.CO;2-O;
RA   Wang J., Lobito A.A., Shen F., Hornung F., Winoto A., Lenardo M.J.;
RT   "Inhibition of Fas-mediated apoptosis by the B cell antigen receptor
RT   through c-FLIP.";
RL   Eur. J. Immunol. 30:155-163(2000).
CC   -!- FUNCTION: Apoptosis regulator protein which may function as a
CC       crucial link between cell survival and cell death pathways in
CC       mammalian cells. Acts as an inhibitor of TNFRSF6 mediated
CC       apoptosis. A proteolytic fragment (p43) is likely retained in the
CC       death-inducing signaling complex (DISC) thereby blocking further
CC       recruitment and processing of caspase-8 at the complex. Full
CC       length and shorter isoforms have been shown either to induce
CC       apoptosis or to reduce TNFRSF-triggered apoptosis. Lacks enzymatic
CC       (caspase) activity (By similarity).
CC   -!- SUBUNIT: TNFRSF6 stimulation triggers recruitment to the death-
CC       inducing signaling complex (DISC) formed by TNFRSF6, FADD and
CC       caspase-8. A proteolytic fragment (p43) stays associated with the
CC       DISC (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=FLIP-L, CASH alpha;
CC         IsoId=O35732-1; Sequence=Displayed;
CC       Name=2; Synonyms=FLIP-S, CASH beta;
CC         IsoId=O35732-2; Sequence=VSP_000842, VSP_000843;
CC   -!- TISSUE SPECIFICITY: Highly expressed in heart.
CC   -!- DEVELOPMENTAL STAGE: At embryonic days E9.5 and E10.5 highest
CC       expression in developping heart.
CC   -!- INDUCTION: Isoform 1 but not isoform 2 is activated by BCR cross-
```

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CC       linking in primary B-cells.
CC   -!- DOMAIN: The caspase domain lacks the active sites residues
CC       involved in catalysis.
CC   -!- PTM: Proteolytically processed; probably by caspase-8. Processing
CC       likely occurs at the DISC, generates subunit p43 and p12 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the peptidase C14 family.
CC   -!- SIMILARITY: Contains 2 death effector (DED) domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y14041; CAA74368.1; -.
DR   EMBL; Y14042; CAA74369.1; -.
DR   EMBL; U97076; AAC53281.1; -.
DR   HSSP; Q9C0K4; 1QTN.
DR   MEROPS; C14.974; -.
DR   MGD; MGI:1336166; Cflar.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR001309; ICE_p20.
DR   Pfam; PF01335; DED; 2.
DR   Pfam; PF00656; Peptidase_C14; 1.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
KW   Alternative splicing; Apoptosis; Repeat.
FT   CHAIN         1    380       CASP8 and FADD-like apoptosis regulator
FT                                subunit p43 (By similarity).
FT   CHAIN       381    484       CASP8 and FADD-like apoptosis regulator
FT                                subunit p12 (By similarity).
FT   DOMAIN        6     78       DED 1.
FT   DOMAIN       97    175       DED 2.
FT   DOMAIN      268    363       Caspase.
FT   DOMAIN      421    425       Poly-Ser.
FT   VARSPLIC    208    218       LQNGRSKEPRF -> VSLEPVYGVPA (in isoform
FT                                2).
FT                                /FTId=VSP_000842.
FT   VARSPLIC    219    480       Missing (in isoform 2).
FT                                /FTId=VSP_000843.
FT   CONFLICT    123    125       Missing (in Ref. 2).
SQ   SEQUENCE   484 AA;  55245 MW;  0BF7A92CB09F5F1F CRC64;

  Query Match            74.9%;  Score 390;  DB 1;  Length 484;
  Best Local Similarity  75.2%;  Pred. No. 2.9e-28;
  Matches   79;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAE 60
              :| :|||||||||| || |||||:|||||||  ::  |||||||| | |||:||   |||
Db          3 QSPVSAEVIHQVEECLDEDEKEMMLFLCRDVTENLAAPNVRDLLDSLSERGQLSFATLAE 62

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||||||||||||| |:  || || ||||||||||||: ||||
Db         63 LLYRVRRFDLLKRILKTDKATVEDHLRRNPHLVSDYRVLLMEIGE 107


RESULT 7
Q6NTR7
ID   Q6NTR7      PRELIMINARY;      PRT;   497 AA.
AC   Q6NTR7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RA   Klein S., Strausberg R.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC068888; AAH68888.1; -.
DR   HSSP; P55211; 1JXQ.
DR   GO; GO:0030693; F:caspase activity; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR001309; ICE_p20.
DR   InterPro; IPR002398; Peptidase_C14.
DR   Pfam; PF01335; DED; 2.
DR   PRINTS; PR00376; IL1BCENZYME.
DR   SMART; SM00115; CASc; 1.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   497 AA;  56872 MW;  1872F291010F83BF CRC64;

  Query Match            29.7%;  Score 154.5;  DB 2;  Length 497;
  Best Local Similarity  38.8%;  Pred. No. 3.6e-06;
  Matches   38;  Conservative   15;  Mismatches   42;  Indels    3;  Gaps    1;

Qy          8 VIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRR 67
              :: |: : ||  | | :||||||   :    ||||||: : :        |||:|| ::|
Db         50 ILLQISDELDAAESEAILFLCRD---NSSKTNVRDLLEDINDYSSPIPFGLAEVLYVIKR 106

Qy         68 FDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||||: |   :  ||  |      :   || ||  | |
Db        107 FDLLKKYLHTSKATVENLLKSRSSIPFSYRSLMVGISE 144


RESULT 8
Q8UVG5
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ID   Q8UVG5      PRELIMINARY;      PRT;   418 AA.
AC   Q8UVG5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Clarp1.
GN   Name=cflar;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98021435; PubMed=9380701; DOI=10.1073/pnas.94.20.10717;
RA   Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
RT   "CLARP, a death effector domain-containing protein interacts with
RT   caspase-8 and regulates apoptosis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20373792; PubMed=10917738;
RA   Inohara N., Nunez G.;
RT   "Genes with homology to mammalian apoptosis regulators identified in
RT   zebrafish.";
RL   Cell Death Differ. 7:509-510(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Inohara N., Nunez G.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF448261; AAL41007.1; -.
DR   HSSP; P55210; 1I4O.
DR   ZFIN; ZDB-GENE-030826-3; cflar.
DR   GO; GO:0030693; F:caspase activity; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   Pfam; PF01335; DED; 2.
DR   SMART; SM00115; CASc; 1.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
SQ   SEQUENCE   418 AA;  47618 MW;  C2ECB3AE571E0237 CRC64;

  Query Match             28.4%;  Score 148;  DB 2;  Length 418;
  Best Local Similarity   32.4%;  Pred. No. 1.2e-05;
  Matches   34;  Conservative   34;  Mismatches   29;  Indels    8;  Gaps    4;

Qy          8 VIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVR-DLLDILRER----GKLSVGD--LAE 60
              ::::|  :| :|| ::||:|| |:  :     :| |||   ::     |:   |: | | |
Db          8 LVNKVTASLSSDESKILLYLCTDLFNNSCVEELRGDLLAFAQQNPNQAGQPHSGNALLME 67

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |:::::|:|||:::   ::: ||  :||   ::|||||||::: |
Db         68 LMFQMKRYDLLRKVFGTNKQQVE-GILRKERVISDYRVLMADVSE 111


RESULT 9
P88961
ID   P88961      PRELIMINARY;      PRT;   188 AA.
AC   P88961;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   ORF K13; ORF K13; v-FLIP (Putative apoptosis inhibitor protein) (FLICE
DE   inhibitory protein).
GN   Name=ORF 71;
OS   Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Gammaherpesvirinae; Rhadinovirus.
OX   NCBI_TaxID=37296;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97094384; PubMed=8939871; DOI=10.1126/science.274.5293.1739;
RA   Moore P.S., Boshoff C., Weiss R.A., Chang Y.;
RT   "Molecular mimicry of human cytokine and cytokine response pathway
RT   genes by KSHV.";
RL   Science 274:1739-1744(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97121480; PubMed=8962146; DOI=10.1073/pnas.93.25.14862;
RA   Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,
RA   Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RT   "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
RT   (HHV8).";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,
RA   Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99329221; PubMed=10400794;
RA   Glenn M., Rainbow L., Aurad F., Davison A., Schulz T.F.;
RT   "Identification of a spliced gene from Kaposi's sarcoma-associated
RT   herpesvirus encoding a protein with similarities to latent membrane
RT   proteins 1 and 2A of Epstein-Barr virus.";
RL   J. Virol. 73:6953-6963(1999).
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Glenn M.A., Rainbow L., Aurade F., Davison A.J., Schulz T.F.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Neipel F., Albrecht J., Fleckenstein B.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97242415; PubMed=9087414;
RA   Thome M., Schneider P., Hofmann K., Fickenscher H., Meinl E.,
RA   Neipel F., Mattmann C., Burns K., Bodmer J.L., Schroter M.,
RA   Scaffidi C., Krammer P.H., Peter M.E., Tschopp J.;
RT   "Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced by
RT   death receptors.";
RL   Nature 386:517-521(1997).
RN   [8]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97296220; PubMed=9151804;
RA   Neipel F., Albrecht J.C., Fleckenstein B.;
RT   "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
RT   human herpesvirus 8: determinants of its pathogenicity?";
RL   J. Virol. 71:4187-4192(1997).
RN   [9]
RP   SEQUENCE FROM N.A.
RA   Neipel F., Albrecht J.-C., Ensser A., Huang Y.-Q., Li J.J.,
RA   Friedman-Kien A.E., Fleckenstein B.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U75698; AAC57156.1; -.
DR   EMBL; AF148805; AAD46498.1; -.
DR   EMBL; U90534; AAB51072.1; -.
DR   EMBL; U93872; AAB62643.1; -.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   Pfam; PF01335; DED; 2.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS50168; DED; 2.
SQ   SEQUENCE   188 AA;  21474 MW;  37CFE147EAE45371 CRC64;

  Query Match             24.9%;  Score 129.5;  DB 2;  Length 188;
  Best Local Similarity   34.0%;  Pred. No. 0.00028;
  Matches   35;  Conservative   23;  Mismatches   38;  Indels    7;  Gaps    3;

Qy          7 EVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILR---ERGKLSVGDLAELLY 63
```

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              ||: :|   | ||::|::|||   : : :  | :  |:  ||   | |:|:   ||| |:
Db          5 EVLCEVARKLGTDDREVVLFL---LNVFIPQPTLAQLIGALRALKEEGRLTFPLLAECLF 61

Qy         64 RVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEI-GE 105
              |  | |||: :| :| : :| ||       | |:: :  : ||
Db         62 RAGRRDLLRDLLHLDPRFLERHLAGTMSYFSPYQLTVLHVDGE 104


RESULT 10
CFLA_MCV1
ID   CFLA_MCV1      STANDARD;      PRT;   241 AA.
AC   Q98325; O11298;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Viral CASP8 and FADD-like apoptosis regulator (v-CFLAR) (Viral FLICE-
DE   inhibitory protein) (v-FLIP).
GN   Name=159L; Synonyms=H-H2.2;
OS   Molluscum contagiosum virus subtype 1 (MCVI).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Molluscipoxvirus.
OX   NCBI_TaxID=10280;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96325459; PubMed=8670425;
RA   Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
RA   Moss B.;
RT   "Genome sequence of a human tumorigenic poxvirus: prediction of
RT   specific host response-evasion genes.";
RL   Science 273:813-816(1996).
RN   [2]
RP   SEQUENCE OF 91-241 FROM N.A.
RX   MEDLINE=97352177; PubMed=9208457; DOI=10.1023/A:1007991508159;
RA   Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
RA   Lopez-Estebaranz J.L., Esteban M., Martin-Gallardo A.;
RT   "A random DNA sequencing, computer-based approach for the generation
RT   of a gene map of Molluscum contagiosum virus.";
RL   Virus Genes 14:73-80(1997).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=97242415; PubMed=9087414;
RA   Thome M., Schneider P., Hofmann K., Fickenscher H., Meinl E.,
RA   Neipel F., Mattmann C., Burns K., Bodmer J.-L., Schroeter M.,
RA   Scaffidi C., Krammer P.H., Peter M.E., Tschopp J.;
RT   "Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced by
RT   death receptors.";
RL   Nature 386:517-521(1997).
RN   [4]
RP   FUNCTION.
RX   MEDLINE=97188440; PubMed=9037025; DOI=10.1073/pnas.94.4.1172;
RA   Bertin J., Armstrong R.C., Ottilie S., Martin D.A., Wang Y., Banks S.,
RA   Wang G.-H., Senkevich T.G., Alnemri E.S., Moss B., Lenardo M.J.,
RA   Tomaselli K.J., Cohen J.I.;
RT   "Death effector domain-containing herpesvirus and poxvirus proteins
RT   inhibit both Fas- and TNFR1-induced apoptosis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:1172-1176(1997).
RN   [5]
RP   CHARACTERIZATION.
RX   MEDLINE=99457304; PubMed=10526240;
RA   Tsukumo S.I., Yonehara S.;
RT   "Requirement of cooperative functions of two repeated death effector
RT   domains in caspase-8 and in MC159 for induction and inhibition of
RT   apoptosis, respectively.";
RL   Genes Cells 4:541-549(1999).
CC   -!- FUNCTION: Inhibits TNFRSF1A, TNFRSF6 and TNFRSF12 induced
CC       apoptosis. May interfere with caspase-8 recruitment and activation
CC       at the death-inducing signaling complex (DISC). May lead to higher
CC       virus production and contribute to virus persistence and
CC       oncogenicity.
CC   -!- SUBUNIT: Associates with the death-inducing signaling complex
CC       (DISC) formed by TNFRSF6, FADD and caspase-8. Interacts with FADD.
CC   -!- SIMILARITY: Contains 2 death effector (DED) domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U60315; AAC55287.1; -.
DR   EMBL; U86888; AAB57923.1; -.
DR   PIR; T30761; T30761.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   Pfam; PF01335; DED; 2.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS50168; DED; 2.
KW   Apoptosis; Repeat.
FT   DOMAIN       8     78       DED 1.
FT   DOMAIN       95    175      DED 2.
SQ   SEQUENCE   241 AA;  26939 MW;  155C9FB0B969E216 CRC64;

  Query Match             23.3%;  Score 121.5;  DB 1;  Length 241;
  Best Local Similarity   36.5%;  Pred. No. 0.002;
  Matches   35;  Conservative   16;  Mismatches   40;  Indels    5;  Gaps    3;

Qy         10 HQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFD 69
              | :|| ||: |  :||||| | |       |   |  | :: ||::  | |:|| ::| |
Db         15 HLLEE-LDSHEDSLLLFLCHDAAPGCT--TVTQALCSLSQQRKLTLAALVEMLYVLQRMD 71

Qy         70 LLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              |||    : ::  |   |     :: || ||  :||
Db         72 LLKSRFGLSKEGAEQ--LLGTSFLTRYRKLMVCVGE 105


RESULT 11
Q66I19
ID   Q66I19      PRELIMINARY;      PRT;   476 AA.
AC   Q66I19;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Caspase 8.
GN   Name=casp8;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
```

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RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RA   Director MGC Project;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC081583; AAH81583.1; -.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR002138; ICE_p10.
DR   InterPro; IPR001309; ICE_p20.
DR   InterPro; IPR002398; Peptidase_C14.
DR   Pfam; PF01335; DED; 2.
DR   PRINTS; PR00376; IL1BCENZYME.
DR   SMART; SM00115; CASc; 1.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS01122; CASPASE_CYS; 1.
DR   PROSITE; PS50207; CASPASE_P10; 1.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
SQ   SEQUENCE   476 AA;  54963 MW;  2EA22110F14C1E01 CRC64;

  Query Match             23.0%;  Score 120;  DB 2;  Length 476;
  Best Local Similarity   33.6%;  Pred. No. 0.006;
  Matches   38;  Conservative   23;  Mismatches   36;  Indels   16;  Gaps    5;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVP-------PNVRDLLDILRERGKLSVG 56
              |  :: |:::| | : : : | |||    :| :|        : :||:  | |:| |
Db          1 MDPQIFHEIDENLTSGDVDQLKFLC----LDFIPKRRLESVTDAKDLILRLDEQGLLEDE 56

Qy         57 DL-AELLYRVRRFDLLKRILKMDRKAVETHLLRNPHL---VSDYRVLMSEIGE 105
              |  |||  : | |||: |||  :: || :|||  :    || || :: :| |
Db         57 LLFPELLITIGRIDLLE-ILKKSKEEVERNLLRCDNSRKGVSAYRKMLLKISE 108


RESULT 12
Q9I8J3
ID   Q9I8J3      PRELIMINARY;      PRT;   476 AA.
AC   Q9I8J3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Caspase-8.
GN   Name=casp8;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20373792; PubMed=10917738;
RA   Inohara N., Nunez G.;
RT   "Genes with homology to mammalian apoptosis regulators identified in
RT   zebrafish.";
RL   Cell Death Differ. 7:509-510(2000).
CC   -!- SIMILARITY: Belongs to the peptidase C14 family.
DR   EMBL; AF273220; AAF79207.1; -.
DR   HSSP; Q9C0K4; 1QTN.
DR   ZFIN; ZDB-GENE-000713-1; casp8.
DR   GO; GO:0030693; F:caspase activity; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR002138; ICE_p10.
DR   InterPro; IPR001309; ICE_p20.
DR   InterPro; IPR002398; Peptidase_C14.
DR   Pfam; PF01335; DED; 2.
DR   PRINTS; PR00376; IL1BCENZYME.
DR   SMART; SM00115; CASc; 1.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS01122; CASPASE_CYS; 1.
DR   PROSITE; PS50207; CASPASE_P10; 1.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
SQ   SEQUENCE   476 AA;  54889 MW;  FD9DFF4B3C3C1FB9 CRC64;

  Query Match             23.0%;  Score 120;  DB 2;  Length 476;
  Best Local Similarity   33.6%;  Pred. No. 0.006;
  Matches   38;  Conservative   23;  Mismatches   36;  Indels   16;  Gaps    5;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVP-------PNVRDLLDILRERGKLSVG 56
              |  :: |:::| | : : : | |||    :| :|        : :||:  | |:| |
Db          1 MDPQIFHEIDENLTSGDVDQLKFLC----LDFIPKRRLESVTDAKDLILRLDEQGLLEDE 56

Qy         57 DL-AELLYRVRRFDLLKRILKMDRKAVETHLLRNPHL---VSDYRVLMSEIGE 105
              |  |||  : | |||: |||  :: || :|||  :    || || :: :| |
Db         57 LLFPELLIAIGRIDLLE-ILKKSKEEVERNLLRCDNSRKGVSAYRKMLLKISE 108


RESULT 13
O11300
ID   O11300      PRELIMINARY;      PRT;   369 AA.
AC   O11300;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein H-K.1 (Fragment).
GN   Name=H-K.1;
OS   Molluscum contagiosum virus subtype 1 (MCVI).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Molluscipoxvirus.
OX   NCBI_TaxID=10280;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97352177; PubMed=9208457; DOI=10.1023/A:1007991508159;
RA   Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
RA   Lopez-Estebaranz J.L., Esteban M., Martin-Gallardo A.;
RT   "A random DNA sequencing, computer-based approach for the generation
RT   of a gene map of molluscum contagiosum virus.";
RL   Virus Genes 14:73-80(1997).
DR   EMBL; U86889; AAB57924.1; -.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   Pfam; PF01335; DED; 2.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS50168; DED; 2.
KW   Hypothetical protein.
FT   NON_TER     369    369
SQ   SEQUENCE   369 AA;  38403 MW;  FECD119A576FF001 CRC64;

  Query Match             22.8%;  Score 119;  DB 2;  Length 369;
  Best Local Similarity   38.6%;  Pred. No. 0.0056;
  Matches   34;  Conservative   12;  Mismatches   38;  Indels    4;  Gaps    2;

Qy         16 LDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRIL 75
              ||  | |:| |||||||         | |  |: |  |::  :||||  :||||:||
Db         18 LDASEHEVLRFLCRDVA--PASKTAEDALRALQRRRLLTLSSMAELLCALRRFDVLKVRF 75

Qy         76 KMDRKAVETHLLRNPHLVSDYRVLMSEI 103
              | |:      |     :| ||: :: |
Db         76 GMTRECAGR--LLGHGFLSQYRLQVAAI 101


RESULT 14
Q98326
ID   Q98326      PRELIMINARY;      PRT;   371 AA.
AC   Q98326;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   MC160L.
GN   Name=MC160L;
OS   Molluscum contagiosum virus subtype 1 (MCVI).
```

```
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Molluscipoxvirus.
OX   NCBI_TaxID=10280;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96325459; PubMed=8670425;
RA   Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
RA   Moss B.;
RT   "Genome sequence of a human tumorigenic poxvirus: prediction of
RT   specific host response-evasion genes.";
RL   Science 273:813-816(1996).
DR   EMBL; U60315; AAC55288.1; -.
DR   PIR; T30762; T30762.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   Pfam; PF01335; DED; 2.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS50168; DED; 2.
SQ   SEQUENCE   371 AA;  38625 MW;  48123BADD29667AB CRC64;

  Query Match             22.8%;  Score 119;  DB 2;  Length 371;
  Best Local Similarity   38.6%;  Pred. No. 0.0056;
  Matches   34;  Conservative   12;  Mismatches   38;  Indels    4;  Gaps    2;

Qy         16 LDTDEKEMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDLAELLYRVRRFDLLKRIL 75
              ||  | |:| |||||||          | |  |: |  |::  :|||  :||||:||
Db         18 LDASEHEVLRFLCRDVA--PASKTAEDALRALQRRRLLTLSSMAELLCALRRFDVLKVRF 75

Qy         76 KMDRKAVETHLLRNPHLVSDYRVLMSEI 103
               | |:      |     :| ||: :: |
Db         76 GMTRECAGR--LLGHGFLSQYRLQVAAI 101


RESULT 15
Q90WU1
ID   Q90WU1      PRELIMINARY;      PRT;   482 AA.
AC   Q90WU1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Caspase 8.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Barton S., Bridgham J.T., Johnson A.L.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the peptidase C14 family.
DR   EMBL; AY057939; AAL23700.1; -.
DR   HSSP; Q9C0K4; 1QDU.
DR   MEROPS; C14.009; -.
DR   GO; GO:0030693; F:caspase activity; IEA.
DR   GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   Pfam; PF01335; DED; 2.
DR   PRINTS; PR00376; IL1BCENZYME.
DR   SMART; SM00115; CASc; 1.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS01122; CASPASE_CYS; 1.
DR   PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
DR   PROSITE; PS50207; CASPASE_P10; 1.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
KW   Hydrolase; Protease; Thiol protease; Zymogen.
SQ   SEQUENCE   482 AA;  54645 MW;  8E3936B6EE090BEF CRC64;

  Query Match             22.2%;  Score 115.5;  DB 2;  Length 482;
  Best Local Similarity   33.0%;  Pred. No. 0.016;
  Matches   36;  Conservative   20;  Mismatches   42;  Indels   11;  Gaps    5;

Qy          6 AEVIHQVEEALDTDEKEMLLFLCRD-VAI----DVVPPNVRDLLDILRERGKLSVGD--- 57
              ::::  : ||||  |   | ||  : | :    |:  |  :     |:|:| : |||
Db          4 SQLLFVISEALDRTELASLKFLSLEHVTVRKREDIEEP--KAFFQALQEKGMIEVGDLFF 61

Qy         58 LAELLYRVRRFDLLKRILKMDRKAVETHL-LRNPHLVSDYRVLMSEIGE 105
              | |||||: | |||   |   |: :|  | :     || :| |: :: |
Db         62 LKELLYRINRIDLLASYLGSSREEMERELQVPGRARVSPFRYLLFQLSE 110


RESULT 16
ICE8_MOUSE
ID   ICE8_MOUSE     STANDARD;      PRT;   480 AA.
AC   O89110; O35669;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Caspase-8 precursor (EC 3.4.22.-) (CASP-8).
GN   Name=Casp8;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   STRAIN=129/SvJ;
RX   MEDLINE=98316661; PubMed=9654089;
RA   Sakamaki K., Tsukumo S.-I., Yonehara S.;
RT   "Molecular cloning and characterization of mouse caspase-8.";
RL   Eur. J. Biochem. 253:399-405(1998).
RN   [2]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX   MEDLINE=99057979; PubMed=9837723; DOI=10.1006/jmbi.1998.2226;
RA   Van de Craen M., Van Loo G., Declercq W., Schotte P.,
RA   van den Brande I., Mandruzzato S., van der Bruggen P., Fiers W.,
RA   Vandenabeele P.;
RT   "Molecular cloning and identification of murine caspase-8.";
RL   J. Mol. Biol. 284:1017-1026(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon, and Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE OF 57-476 FROM N.A.
RA   Kioschis P., Kischkel F., Poustka A., Krammer P.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Most upstream protease of the activation cascade of
CC       caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
CC       induced cell death. Binding to the adapter molecule FADD recruits
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CC       it to either receptor. The resulting aggregate called death-
CC       inducing signaling complex (DISC) performs CASP8 proteolytic
CC       activation. The active dimeric enzyme is then liberated from the
CC       DISC and free to activate downstream apoptotic proteases.
CC       Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CC       CAP5 and CAP6) are likely retained in the DISC. Cleaves and
CC       activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
CC       participate in the GZMB apoptotic pathways. Cleaves ADPRT.
CC       Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
CC       Likely target for the cowpox virus CRMA death inhibitory protein.
CC   -!- ENZYME REGULATION: Inhibited by Z-VAD-FK, Crma and P35.
CC   -!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 10 kDa (p10) subunit.
CC       Interacts with FADD, CFLAR and PEA15 (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues.
CC       Highest expression in spleen, thymus, lung, liver and kidney.
CC       Lower expression in heart, brain, testis and skeletal muscle.
CC   -!- DEVELOPMENTAL STAGE: In the embryo, highest expression occurs at
CC       day 7.
CC   -!- PTM: Generation of the subunits requires association with the
CC       death-inducing signaling complex (DISC), whereas additional
CC       processing is likely due to the autocatalytic activity of the
CC       activated protease. GZMB and CASP10 can be involved in these
CC       processing events (By similarity).
CC   -!- SIMILARITY: Belongs to the peptidase C14 family.
CC   -!- SIMILARITY: Contains 2 death effector (DED) domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF067841; AAC40132.1; -.
DR   EMBL; AF067835; AAC40132.1; JOINED.
DR   EMBL; AF067836; AAC40132.1; JOINED.
DR   EMBL; AF067837; AAC40132.1; JOINED.
DR   EMBL; AF067838; AAC40132.1; JOINED.
DR   EMBL; AF067839; AAC40132.1; JOINED.
DR   EMBL; AF067840; AAC40132.1; JOINED.
DR   EMBL; AF067834; AAC40131.1; -.
DR   EMBL; AJ007749; CAA07677.1; -.
DR   EMBL; BC006737; AAH06737.1; -.
DR   EMBL; BC049955; AAH49955.1; -.
DR   EMBL; AJ000641; CAA04196.1; -.
DR   HSSP; Q9C0K4; 1QTN.
DR   MEROPS; C14.009; -.
DR   MGD; MGI:1261423; Casp8.
DR   GO; GO:0005737; C:cytoplasm; IDA.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   GO; GO:0030693; F:caspase activity; IDA.
DR   GO; GO:0006915; P:apoptosis; IDA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR002138; ICE_p10.
DR   InterPro; IPR001309; ICE_p20.
DR   InterPro; IPR002398; Peptidase_C14.
DR   Pfam; PF01335; DED; 2.
DR   Pfam; PF00656; Peptidase_C14; 1.
DR   PRINTS; PR00376; IL1BCENZYME.
DR   PROSITE; PS01122; CASPASE_CYS; 1.
DR   PROSITE; PS01121; CASPASE_HIS; 1.
DR   PROSITE; PS50207; CASPASE_P10; 1.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
KW   Apoptosis; Hydrolase; Repeat; Thiol protease; Zymogen.
FT   PROPEP        1    218       By similarity.
FT   CHAIN       219    376       Caspase-8 subunit p18.
FT   PROPEP      377    387       By similarity.
FT   CHAIN       388    480       Caspase-8 subunit p10.
FT   ACT_SITE    319    319       By similarity.
FT   ACT_SITE    362    362       By similarity.
FT   DOMAIN        3     80       DED 1.
FT   DOMAIN      101    177       DED 2.
FT   CONFLICT     68     71       HISR -> PHPVG (in Ref. 4).
FT   CONFLICT     94     99       DNAQIS -> RQCPRFL (in Ref. 4).
FT   CONFLICT     96     96       A -> V (in Ref. 2).
FT   CONFLICT    103    107       VMLFK -> SCSFR (in Ref. 4).
FT   CONFLICT    475    475       K -> N (in Ref. 4).
SQ   SEQUENCE   480 AA;  55356 MW;  045268AE3DE5ED4F CRC64;

  Query Match             22.0%;  Score 114.5;  DB 1;  Length 480;
  Best Local Similarity   29.4%;  Pred. No. 0.02;
  Matches   32;  Conservative   27;  Mismatches   33;  Indels   17;  Gaps    5;

Qy          9 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLD-------ILRERGKLSVGDLA-- 59
              :: : | | :::   | |||    :| :|   :: ::        |||:| |  |:|:
Db          7 LYAIAEELGSEDLAALKFLC----LDYIPHKKQETIEDAQKLFLRLREKGMLEEGNLSFL 62

Qy         60 -ELLYRVRRFDLLKRILKMDRKAVETHLLRNPH--LVSDYRVLMSEIGE 105
               |||: : |:|||   |  :|: :    ||:|    :| |||:: :: |
Db         63 KELLFHISRWDLLVNFLDCNREEM-VRELRDPDNAQISPYRVMLFKLSE 110


RESULT 17
Q9JHX4
ID   Q9JHX4      PRELIMINARY;      PRT;   482 AA.
AC   Q9JHX4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Caspase-8.
GN   Name=CASP8;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Itoh T., Itoh A., Pleasure D.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA   Cao G., Graham S.H., Chen D., Chen J.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the peptidase C14 family.
DR   EMBL; AF279308; AAF87778.1; -.
DR   EMBL; AF288372; AAK83055.1; -.
DR   HSSP; Q9C0K4; 1QDU.
DR   MEROPS; C14.009; -.
DR   GO; GO:0030693; F:caspase activity; IEA.
DR   GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR002138; ICE_p10.
DR   InterPro; IPR001309; ICE_p20.
DR   InterPro; IPR002398; Peptidase_C14.
DR   Pfam; PF01335; DED; 2.
DR   PRINTS; PR00376; IL1BCENZYME.
DR   SMART; SM00115; CASc; 1.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS01122; CASPASE_CYS; 1.
DR   PROSITE; PS01121; CASPASE_HIS; 1.
DR   PROSITE; PS50207; CASPASE_P10; 1.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
KW   Hydrolase; Protease; Thiol protease; Zymogen.
SQ   SEQUENCE   482 AA;  55339 MW;  82B4A29330C53264 CRC64;
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  Query Match             20.4%;  Score 106.5;  DB 2;  Length 482;
  Best Local Similarity   30.8%;  Pred. No. 0.11;
  Matches   32;  Conservative   21;  Mismatches   44;  Indels    7;  Gaps    3;

Qy          9 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLLDI---LRERGKLSVGDLA---ELL 62
              :: : | |  :|   | ||| |        :: |:| :   |:| | |   :|:   |||
Db          7 LYDIAERLGNEELAALKFLCLDHIPQKKQESINDVLVLFQRLQEEGMLEEDNLSFLKELL 66

Qy         63 YRVRRFDLLKRILKMDRKAVETHL-LRNPHLVSDYRVLMSEIGE 105
              : : | ||| |:||   : :   | :     || |||:: :: |
Db         67 FHISRRDLLSRVLKSSPEEMVRELQVLGKAQVSAYRVMLFKLSE 110


RESULT 18
Q99CX0
ID   Q99CX0      PRELIMINARY;      PRT;   182 AA.
AC   Q99CX0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   V-FLIP.
OS   Bovine herpesvirus 4 (BoHV-4) (Movar virus).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Gammaherpesvirinae; Rhadinovirus.
OX   NCBI_TaxID=10385;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20583805; PubMed=11152491;
RX   DOI=10.1128/JVI.75.3.1186-1194.2001;
RA   Zimmermann W., Broll H., Ehlers B., Buhk H.-J., Rosenthal A.,
RA   Goltz M.;
RT   "Genome sequence of bovine herpesvirus 4, a bovine Rhadinovirus, and
RT   identification of an origin of DNA replication.";
RL   J. Virol. 75:1186-1194(2001).
DR   EMBL; AF318573; AAK07993.1; -.
DR   HSSP; Q9Z297; 1N3K.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   Pfam; PF01335; DED; 2.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS50168; DED; 2.
SQ   SEQUENCE   182 AA;  21792 MW;  73BF1ADD9B0FE6A6 CRC64;

  Query Match             20.1%;  Score 104.5;  DB 2;  Length 182;
  Best Local Similarity   26.4%;  Pred. No. 0.059;
  Matches   28;  Conservative   28;  Mismatches   43;  Indels    7;  Gaps    3;

Qy          4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDL---LDILRERGKLSVGDLAE 60
              :: :|:  :|  |: :||  :::   |     :|    |    |: |  : |:    | |
Db          2 VTRDVLLAIETHLNQNEKTFVMYFLLD---PYIPKECEDFLPTLENLHSKRKIIYPILIE 58

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNP-HLVSDYRVLMSEIGE 105
              |:| ::|||||: |  :| : |:  :  :  : :| |: |:  ||:
Db         59 LMYILQRFDLLRSIFLLDHRFVKDQITSSHWNYISPYKQLIFSIGQ 104


RESULT 19
Q9IB64
ID   Q9IB64      PRELIMINARY;      PRT;   500 AA.
AC   Q9IB64;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Caspase-8.
GN   Name=xCaspase-8;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20209426; PubMed=10744739; DOI=10.1074/jbc.275.14.10484;
RA   Nakajima K., Takahashi A., Yaoita Y.;
RT   "Structure, expression and function of the Xenopus laevis caspase
RT   family.";
RL   J. Biol. Chem. 275:10484-10491(2000).
CC   -!- SIMILARITY: Belongs to the peptidase C14 family.
DR   EMBL; AB038171; BAA94749.1; -.
DR   HSSP; Q9C0K4; 1QTN.
DR   GO; GO:0030693; F:caspase activity; IEA.
DR   GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR002138; ICE_p10.
DR   InterPro; IPR001309; ICE_p20.
DR   InterPro; IPR000226; Interleukin_7_9.
DR   InterPro; IPR002398; Peptidase_C14.
DR   Pfam; PF01335; DED; 2.
DR   PRINTS; PR00376; IL1BCENZYME.
DR   SMART; SM00115; CASc; 1.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS01122; CASPASE_CYS; 1.
DR   PROSITE; PS01121; CASPASE_HIS; 1.
DR   PROSITE; PS50207; CASPASE_P10; 1.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
DR   PROSITE; PS00255; INTERLEUKIN_7_9; UNKNOWN_1.
KW   Hydrolase; Protease; Thiol protease; Zymogen.
SQ   SEQUENCE   500 AA;  57623 MW;  AE138D4145108AE2 CRC64;

  Query Match             20.1%;  Score 104.5;  DB 2;  Length 500;
  Best Local Similarity   27.6%;  Pred. No. 0.18;
  Matches   29;  Conservative   27;  Mismatches   42;  Indels    7;  Gaps    3;

Qy          7 EVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRD---LLDILRERGKLSVGDLA---E 60
              ::: :: | ||  |   ::|||          |::|   |   |:::  :   ||:   |
Db         19 KLLFEISEDLDKTETLAMIFLCEKRVTAQEKENIKDAKTLFLCLKKKDLICYNDLSFLKE 78

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              ||||: | |||:  | :  : ::  :  :|  :| ||:|: :| :
Db         79 LLYRIGRNDLLRGKLGVRTEEIKRIIEVSPQ-ISPYRILLYDISQ 122


RESULT 20
CFLA_EHV2
ID   CFLA_EHV2      STANDARD;      PRT;   171 AA.
AC   Q66674;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Viral CASP8 and FADD-like apoptosis regulator (v-CFLAR) (Viral FLICE-
DE   inhibitory protein) (v-FLIP).
GN   Name=E8;
OS   Equine herpesvirus 2 (strain 86/87) (EHV-2).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Gammaherpesvirinae; Rhadinovirus.
OX   NCBI_TaxID=82831;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95302501; PubMed=7783207;
RA   Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
RT   "The DNA sequence of equine herpesvirus 2.";
RL   J. Mol. Biol. 249:520-528(1995).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=97242415; PubMed=9087414;
RA   Thome M., Schneider P., Hofmann K., Fickenscher H., Meinl E.,
RA   Neipel F., Mattmann C., Burns K., Bodmer J.-L., Schroeter M.,
RA   Scaffidi C., Krammer P.H., Peter M.E., Tschopp J.;
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RT   "Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced by
RT   death receptors.";
RL   Nature 386:517-521(1997).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=97188440; PubMed=9037025; DOI=10.1073/pnas.94.4.1172;
RA   Bertin J., Armstrong R.C., Ottilie S., Martin D.A., Wang Y., Banks S.,
RA   Wang G.-H., Senkevich T.G., Alnemri E.S., Moss B., Lenardo M.J.,
RA   Tomaselli K.J., Cohen J.I.;
RT   "Death effector domain-containing herpesvirus and poxvirus proteins
RT   inhibit both Fas- and TNFR1-induced apoptosis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:1172-1176(1997).
CC   -!- FUNCTION: Inhibits TNFRSF1A, TNFRSF6, TNFRSF10 and TNFRSF12
CC       induced apoptosis. May interfere with caspase-8 recruitment and
CC       activation at the death-inducing signaling complex (DISC). May
CC       lead to higher virus production and contribute to virus
CC       persistence and oncogenicity.
CC   -!- SUBUNIT: Associates with the death-inducing signaling complex
CC       (DISC) formed by TNFRSF6, FADD and caspase-8. Interacts with FADD.
CC   -!- SIMILARITY: Contains 2 death effector (DED) domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U20824; AAC13862.1; -.
DR   PIR; S55668; S55668.
DR   PDB; 1LGJ; Model; A=4-171.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   Pfam; PF01335; DED; 2.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS50168; DED; 2.
KW   3D-structure; Apoptosis; Repeat.
FT   DOMAIN       1     74       DED 1.
FT   DOMAIN      92    171       DED 2.
SQ   SEQUENCE   171 AA;  19925 MW;  4CEAF9D0EE04D9AE CRC64;

  Query Match             19.1%;  Score 99.5;  DB 1;  Length 171;
  Best Local Similarity   39.4%;  Pred. No. 0.16;
  Matches   26;  Conservative    8;  Mismatches   21;  Indels   11;  Gaps    2;

Qy          15 ALDTDEKEMLLFLCRDVAIDVVPPN------VRDLLDILRERGKLSVGDLAELLYRVRRF 68
               :|| || |  |:||||:       |       ||    | :   ||  :  |||:|| |
Db          12 SLDEDETETYLYLCRDLL-----KNKGEFQCTRDAFKFLSDYACLSAANQMELLFRVGRL 66

Qy          69 DLLKRI 74
               ||::||
Db          67 DLIRRI 72


RESULT 21
Q6NVI2
ID   Q6NVI2      PRELIMINARY;      PRT;   278 AA.
AC   Q6NVI2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC068050; AAH68050.1; -.
DR   GO; GO:0030693; F:caspase activity; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR001309; ICE_p20.
DR   Pfam; PF01335; DED; 2.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   278 AA;  32386 MW;  3918E516CB1A8B40 CRC64;

  Query Match             18.9%;  Score 98.5;  DB 2;  Length 278;
  Best Local Similarity   29.4%;  Pred. No. 0.34;
  Matches   32;  Conservative   26;  Mismatches   34;  Indels   17;  Gaps    6;

Qy           9 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPN----VRDLLDI---LRERGKLSVGDLA-- 59
               :: : | ||:::   | ||    ::| :|      ::| | :   |:|:  |   :|:
Db           7 LYDIGEQLDSEDLASLKFL----SLDYIPQRKQEPIKDALMLFQRLQEKRMLEESNLSFL 62

Qy          60 -ELLYRVRRFDLLKRILKMDRKAVETHLLRNP--HLVSDYRVLMSEIGE 105
                |||:|: | |||   |   :: :|   |: |    :| |||:: :| |
Db          63 KELLFRINRLDLLITYLNTRKEEMERE-LQTPGRAQISAYRVMLYQISE 110


RESULT 22
ICE8_HUMAN
ID   ICE8_HUMAN     STANDARD;      PRT;   479 AA.
AC   Q14790; O14676; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796;
AC   Q15780; Q15806; Q8TDI1; Q8TDI2; Q8TDI3; Q8TDI4; Q8TDI5; Q96T22;
AC   Q9C0K4; Q9UQ81;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Caspase-8 precursor (EC 3.4.22.-) (CASP-8) (ICE-like apoptotic
DE   protease 5) (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous
DE   ICE/CED-3-like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine
DE   protease) (Apoptotic protease Mch-5) (CAP4).
GN   Name=CASP8; Synonyms=MCH5;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 5; 6; 7 AND 8).
RC   TISSUE=B-cell, and Thymus;
RX   MEDLINE=96279826; PubMed=8681376; DOI=10.1016/S0092-8674(00)81265-9;
```

RA Boldin M.P., Goncharov T.M., Goltsev Y.V., Wallach D.;
RT "Involvement of MACH, a novel MORT1/FADD-interacting protease, in
RT Fas/APO-1- and TNF receptor-induced cell death.";
RL Cell 85:803-815(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
RX MEDLINE=96279827; PubMed=8681377; DOI=10.1016/S0092-8674(00)81266-0;
RA Muzio M., Chinnaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,
RA Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
RA Krammer P.H., Peter M.E., Dixit V.M.;
RT "FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited
RT to the CD95 (Fas/APO-1) death-inducing signaling complex.";
RL Cell 85:817-827(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RC TISSUE=T-cell;
RX MEDLINE=96353838; PubMed=8755496; DOI=10.1073/pnas.93.15.7464;
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J.F., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99132295; PubMed=9931493; DOI=10.1016/S0378-1119(98)00565-4;
RA Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.;
RT "Structure and chromosome localization of the human CASP8 gene.";
RL Gene 226:225-232(1999).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=97373543; PubMed=9228018; DOI=10.1074/jbc.272.30.18542;
RA Srinivasula S.M., Ahmad M., Ottilie S., Bullrich F., Banks S.,
RA Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
RA Armstrong R.C., Alnemri E.S.;
RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
RT Fas/TNFR1-induced apoptosis.";
RL J. Biol. Chem. 272:18542-18545(1997).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=21100893; PubMed=11161814; DOI=10.1006/geno.2000.6392;
RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA Ikeda J.-E., Hayden M.R.;
RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RT critical region at chromosome 2q33-q34: candidate genes for ALS2.";
RL Genomics 71:200-213(2001).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 7), AND FUNCTION OF ISOFORM 7.
RC TISSUE=Leukocyte;
RX MEDLINE=22005982; PubMed=12010809; DOI=10.1182/blood.V99.11.4070;
RA Himeji D., Horiuchi T., Tsukamoto H., Hayashi K., Watanabe T.,
RA Harada M.;
RT "Characterization of caspase-8L: a novel isoform of caspase-8 that
RT behaves as an inhibitor of the caspase cascade.";
RL Blood 99:4070-4078(2002).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 9), AND INTERACTION OF ISOFORM 9
RP WITH BCAP31 AT THE ENDOPLASMIC RETICULUM.
RX MEDLINE=21927603; PubMed=11917123; DOI=10.1073/pnas.072088099;
RA Breckenridge D.G., Nguyen M., Kuppig S., Reth M., Shore G.C.;
RT "The procaspase-8 isoform, procaspase-8L, recruited to the BAP31
RT complex at the endoplasmic reticulum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 7).
RC TISSUE=Leukocyte;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP PARTIAL SEQUENCE, AND PROCESSING.
RX MEDLINE=97121412; PubMed=8962078; DOI=10.1073/pnas.93.25.14486;
RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RA Alnemri E.S.;
RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
RT protease Mch5 is a CrmA-inhibitable protease that activates multiple
RT Ced-3/ICE-like cysteine proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
RN [11]
RP FUNCTION.
RX MEDLINE=97160607; PubMed=9006941; DOI=10.1074/jbc.272.5.2952;
RA Muzio M., Salvesen G.S., Dixit V.M.;
RT "FLICE induced apoptosis in a cell-free system. Cleavage of caspase
RT zymogens.";
RL J. Biol. Chem. 272:2952-2956(1997).
RN [12]
RP PROCESSING.
RX MEDLINE=97327557; PubMed=9184224; DOI=10.1093/emboj/16.10.2794;
RA Medema J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,
RA Krammer P.H., Peter M.E.;
RT "FLICE is activated by association with the CD95 death-inducing
RT signaling complex (DISC).";
RL EMBO J. 16:2794-2804(1997).
RN [13]
RP CHARACTERIZATION OF ISOFORM 7.
RX MEDLINE=20318377; PubMed=10860845; DOI=10.1006/bbrc.2000.2841;
RA Horiuchi T., Himeji D., Tsukamoto H., Harashima S., Hashimura C.,
RA Hayashi K.;
RT "Dominant expression of a novel splice variant of caspase-8 in human
RT peripheral blood lymphocytes.";
RL Biochem. Biophys. Res. Commun. 272:877-881(2000).
RN [14]
RP INTERACTIONS WITH BCL2; BCL2L1 AND BCAP31.
RX MEDLINE=97477382; PubMed=9334338; DOI=10.1083/jcb.139.2.327;
RA Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
RA Cromlish J.A., Shore G.C.;
RT "p28 Bap31, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the
RT endoplasmic reticulum.";
RL J. Cell Biol. 139:327-338(1997).
RN [15]
RP INTERACTION WITH PEA15.
RX MEDLINE=99369240; PubMed=10442631; DOI=10.1038/sj.onc.1202831;
RA Condorelli G., Vigliotta G., Cafieri A., Trencia A., Andalo P.,
RA Oriente F., Miele C., Caruso M., Formisano P., Beguinot F.;
RT "PED/PEA-15: an anti-apoptotic molecule that regulates FAS/TNFR1-
RT induced apoptosis.";
RL Oncogene 18:4409-4415(1999).
RN [16]
RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E.;
RT "An unappreciated role for RNA surveillance.";
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=99451259; PubMed=10508784; DOI=10.1016/S0969-2126(99)80179-8;

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RA   Blanchard H., Kodandapani L., Mittl P.R.E., Di Marco S., Krebs J.F.,
RA   Wu J.C., Tomaselli K.J., Gruetter M.G.;
RT   "The three-dimensional structure of caspase-8: an initiator enzyme in
RT   apoptosis.";
RL   Structure 7:1125-1133(1999).
RN   [18]
RP   VARIANT CASP8D TRP-248.
RX   MEDLINE=22239940; PubMed=12353035; DOI=10.1038/nature01063;
RA   Chun H.J., Zheng L., Ahmad M., Wang J., Speirs C.K., Siegel R.M.,
RA   Dale J.K., Puck J., Davis J., Hall C.G., Skoda-Smith S.,
RA   Atkinson T.P., Straus S.E., Lenardo M.J.;
RT   "Pleiotropic defects in lymphocyte activation caused by caspase-8
RT   mutations lead to human immunodeficiency.";
RL   Nature 419:395-399(2002).
CC   -!- FUNCTION: Most upstream protease of the activation cascade of
CC       caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
CC       induced cell death. Binding to the adapter molecule FADD recruits
CC       it to either receptor. The resulting aggregate called death-
CC       inducing signaling complex (DISC) performs CASP8 proteolytic
CC       activation. The active dimeric enzyme is then liberated from the
CC       DISC and free to activate downstream apoptotic proteases.
CC       Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CC       CAP5 and CAP6) are likely retained in the DISC. Cleaves and
CC       activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
CC       participate in the GZMB apoptotic pathways. Cleaves ADPRT.
CC       Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
CC       Likely target for the cowpox virus CRMA death inhibitory protein.
CC       Isoforms 5, 6, 7 and 8 lack the catalytic site and may interfere
CC       with the pro-apoptotic activity of the complex.
CC   -!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 10 kDa (p10) subunit.
CC       Interacts with FADD, CFLAR and PEA15. Isoform 9 interacts at the
CC       endoplasmic reticulum with a complex containing BCAP31, BAP29,
CC       BCL2 and/or BCL2L1.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.

  Query Match             18.9%;  Score 98.5;  DB 1;  Length 479;
  Best Local Similarity   29.4%;  Pred. No. 0.63;
  Matches   32;  Conservative   26;  Mismatches   34;  Indels   17;  Gaps    6;

Qy          9 IHQVEEALDTDEKEMLLFLCRDVAIDVVPPN----VRDLLDI---LRERGKLSVGDLA-- 59
              :: : | ||::    | ||    ::| :|      ::| | :   |:|:  |   :|:
Db          7 LYDIGEQLDSEDLASLKFL----SLDYIPQRKQEPIKDALMLFQRLQEKRMLEESNLSFL 62

Qy         60 -ELLYRVRRFDLLKRILKMDRKAVETHLLRNP--HLVSDYRVLMSEIGE 105
               |||:|: | |||    |   :: :|   |: |    :| |||:: :| |
Db         63 KELLFRINRLDLLITYLNTRKEEMERE-LQTPGRAQISAYRVMLYQISE 110


RESULT 23
Q6PAD9
ID   Q6PAD9      PRELIMINARY;      PRT;   512 AA.
AC   Q6PAD9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MGC68465 protein.
GN   Name=MGC68465;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the peptidase C14 family.
DR   EMBL; BC060356; AAH60356.1; -.
DR   HSSP; P55210; 1K86.
DR   GO; GO:0030693; F:caspase activity; IEA.
DR   GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR002138; ICE_p10.
DR   InterPro; IPR001309; ICE_p20.
DR   InterPro; IPR002398; Peptidase_C14.
DR   Pfam; PF01335; DED; 2.
DR   PRINTS; PR00376; IL1BCENZYME.
DR   SMART; SM00115; CASc; 1.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS01122; CASPASE_CYS; 1.
DR   PROSITE; PS01121; CASPASE_HIS; 1.
DR   PROSITE; PS50207; CASPASE_P10; 1.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
KW   Hydrolase; Protease; Thiol protease; Zymogen.
SQ   SEQUENCE   512 AA;  58799 MW;  FE91F00AD8C0EFBB CRC64;

  Query Match             17.9%;  Score 93;  DB 2;  Length 512;
  Best Local Similarity   33.3%;  Pred. No. 2.2;
  Matches   34;  Conservative   18;  Mismatches   38;  Indels   12;  Gaps    5;

Qy         12 VEEALDTDEKEMLLFLCRDVAIDVVPPNVR---DLLDILRERGKLSVGD---LAELLYRV 65
              ::: |  :: | | ||||||       :||   :|   |:    :|  |   |||||| :
Db         10 IDDGLGREDIEALKFLCRDVLRKNKLLSVRSGQELFQQLKTEDLISEDDFFLLAELLYII 69

Qy         66 RRFDLLKRILKMDRKAVETHLLRNPH--LVSDYRVLMSEIGE 105
                 || | |  ::: |:  |   ||   :| || :: |: |
Db         70 NHHSLL-RDLGTNKENVQKDL---PHQGKISSYRRMLYELSE 107


RESULT 24
FADD_HUMAN
ID   FADD_HUMAN     STANDARD;      PRT;   208 AA.
AC   Q13158; Q14866;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
```

```
DE   FADD protein (FAS-associating death domain-containing protein)
DE   (Mediator of receptor induced toxicity).
GN   Name=FADD; Synonyms=MORT1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS.
RC   TISSUE=Umbilical vein endothelial cells;
RX   MEDLINE=95277837; PubMed=7538907; DOI=10.1016/0092-8674(95)90071-3;
RA   Chinnaiyan A.M., O'Rourke K., Tewari M., Dixit V.M.;
RT   "FADD, a novel death domain-containing protein, interacts with the
RT   death domain of Fas and initiates apoptosis.";
RL   Cell 81:505-512(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95229578; PubMed=7536190; DOI=10.1074/jbc.270.14.7795;
RA   Boldin M.P., Varfolomeev E.E., Pancer Z., Mett I.L., Camonis J.H.,
RA   Wallach D.;
RT   "A novel protein that interacts with the death domain of Fas/APO1
RT   contains a sequence motif related to the death domain.";
RL   J. Biol. Chem. 270:7795-7798(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   INTERACTION WITH PEA15.
RX   MEDLINE=99369240; PubMed=10442631; DOI=10.1038/sj.onc.1202831;
RA   Condorelli G., Vigliotta G., Cafieri A., Trencia A., Andalo P.,
RA   Oriente F., Miele C., Caruso M., Formisano P., Beguinot F.;
RT   "PED/PEA-15: an anti-apoptotic molecule that regulates FAS/TNFR1-
RT   induced apoptosis.";
RL   Oncogene 18:4409-4415(1999).
RN   [5]
RP   INTERACTION WITH MBD4.
RX   PubMed=12702765; DOI=10.1073/pnas.0431215100;
RA   Screaton R.A., Kiessling S., Sansom O.J., Millar C.B., Maddison K.,
RA   Bird A., Clarke A.R., Frisch S.M.;
RT   "Fas-associated death domain protein interacts with methyl-CpG binding
RT   domain protein 4: a potential link between genome surveillance and
RT   apoptosis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:5211-5216(2003).
RN   [6]
RP   STRUCTURE BY NMR OF 1-83.
RX   MEDLINE=98241233; PubMed=9582077; DOI=10.1038/31972;
RA   Eberstadt M., Huang B., Chen Z., Meadows R.P., Ng S.C., Zheng L.,
RA   Lenardo M.J., Fesik S.W.;
RT   "NMR structure and mutagenesis of the FADD (Mort1) death-effector
RT   domain.";
RL   Nature 392:941-945(1998).
CC   -!- FUNCTION: Apoptotic adaptor molecule that recruits caspase-8 or
CC       caspase-10 to the activated Fas (CD95) or TNFR-1 receptors. The
CC       resulting aggregate called the death-inducing signaling complex
CC       (DISC) performs caspase-8 proteolytic activation. Active caspase-8
CC       initiates the subsequent cascade of caspases (aspartate-specific
CC       cysteine proteases) mediating apoptosis.
CC   -!- SUBUNIT: Interacts with CFLAR, PEA15 and MBD4.
CC   -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues, except
CC       for peripheral blood mononuclear leukocytes.
CC   -!- DOMAIN: Contains a death domain involved in the binding of the
CC       corresponding domain within Fas receptor.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   -!- SIMILARITY: Contains 1 death effector (DED) domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch)..
CC   ----------------------------------------------------------------------
DR   EMBL; U24231; AAA86517.1; -.
DR   EMBL; X84709; CAA59197.1; -.
DR   EMBL; BC000334; AAH00334.1; -.
DR   PIR; A56912; A56912.
DR   PDB; 1A1W; NMR; @=1-91.
DR   PDB; 1A1Z; NMR; @=1-91.
DR   PDB; 1E3Y; NMR; A=89-192.
DR   PDB; 1E41; NMR; A=89-192.
DR   Genew; HGNC:3573; FADD.
DR   H-InvDB; HIX0009893; -.
DR   MIM; 602457; -.
DR   GO; GO:0005123; F:death receptor binding; TAS.
DR   GO; GO:0004871; F:signal transducer activity; IEP.
DR   GO; GO:0008625; P:induction of apoptosis via death domain rec. . .; TAS.
DR   GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . .; IEP.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   Pfam; PF00531; Death; 1.
DR   Pfam; PF01335; DED; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS50168; DED; 1.
KW   3D-structure; Apoptosis.
FT   DOMAIN        3     81       DED.
FT   DOMAIN       97    181       Death.
FT   MUTAGEN     121    121       V->N: No interaction with Fas receptor.
FT   CONFLICT     32     32       G -> V (in Ref. 2).
FT   HELIX         3     28
FT   TURN         29     31
FT   HELIX        33     38
FT   HELIX        42     52
FT   TURN         53     53
FT   TURN         57     58
FT   HELIX        61     70
FT   TURN         71     71
FT   HELIX        73     81
FT   TURN         96     96
FT   HELIX        97    106
FT   TURN        107    107
FT   HELIX       112    120
FT   HELIX       123    132
FT   TURN        134    135
FT   HELIX       137    152
FT   HELIX       153    155
FT   HELIX       158    167
FT   TURN        168    169
FT   HELIX       171    185
FT   TURN        186    189
SQ   SEQUENCE   208 AA;  23279 MW;  0E65E2F852E83507 CRC64;

  Query Match             15.9%;  Score 83;  DB 1;  Length 208;
  Best Local Similarity   27.6%;  Pred. No. 7.1;
```

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  Matches   29;  Conservative   18;  Mismatches   50;  Indels    8;  Gaps    3;

Qy          8 VIHQVEEALDTDEKEMLLFLCRDVA----IDVVPPNVRDLLDILRERGKLSVGD---LAE 60
              ::| |  :| : |   | |||        :: |   : ||  :| |:  |  |    | |
Db          7 LLHSVSSSLSSSELTELKFLCLGRVGKRKLERVQSGL-DLFSMLLEQNDLEPGHTELLRE 65

Qy         61 LLYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              ||  :|| |||:|:   :  |          | : : |:   :|:
Db         66 LLASLRRHDLLRRVDDFEAGAAAGAAPGEEDLCAAFNVICDNVGK 110


RESULT 25
Q6MDM0
ID   Q6MDM0      PRELIMINARY;      PRT;  1388 AA.
AC   Q6MDM0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Probable DNA-directed RNA polymerase, beta' chain.
GN   Name=rpoC; Synonyms=tabB; OrderedLocusNames=pc0605;
OS   Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC   Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX   NCBI_TaxID=264201;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA   Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
RA   Rattei T., Mewes H.-W., Wagner M.;
RT   "Genome sequence of an amoeba symbiont and its use for reconstructing
RT   the evolutionary history of chlamydiae.";
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX908798; CAF23329.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
DR   GO; GO:0006350; P:transcription; IEA.
DR   InterPro; IPR006592; RNA_polA_N.
DR   InterPro; IPR000722; RNA_pol_A.
DR   InterPro; IPR007080; RNA_pol_Rpb1_1.
DR   InterPro; IPR007066; RNA_pol_Rpb1_3.
DR   InterPro; IPR007083; RNA_pol_Rpb1_4.
DR   InterPro; IPR007081; RNA_pol_Rpb1_5.
DR   Pfam; PF04997; RNA_pol_Rpb1_1; 1.
DR   Pfam; PF00623; RNA_pol_Rpb1_2; 1.
DR   Pfam; PF04983; RNA_pol_Rpb1_3; 1.
DR   Pfam; PF05000; RNA_pol_Rpb1_4; 1.
DR   Pfam; PF04998; RNA_pol_Rpb1_5; 1.
DR   SMART; SM00663; RPOLA_N; 1.
KW   Complete proteome; DNA-directed RNA polymerase.
SQ   SEQUENCE   1388 AA;  155296 MW;  3803E1C156B9F77D CRC64;

  Query Match            15.5%;  Score 81;  DB 2;  Length 1388;
  Best Local Similarity   30.4%;  Pred. No. 88;
  Matches   28;  Conservative   23;  Mismatches   29;  Indels   12;  Gaps    6;

Qy          1 KSRMS-AEVIHQVEEALDTDEK-EMLLFLCRDVAIDVVPPNVRDLLDILRERGKLSVGDL 58
              ::||  |: :  :|  : :| | | ::  |    : |:||::| |: :  : |: :  ||
Db        208 QARMKLAKRLKIIESFVSSDNKPEWMIMSC----VPVIPPDLRPLVPL--DGGRFATSDL 261

Qy         59 AELLYRV-RRFDLLKRILKMDRKAVETHLLRN 89
               :|  ||  | : || |||:    |   ::||
Db        262 NDLYRRVINRNNRLKAILKLKTPDV---IVRN 290


RESULT 26
Q68HC0
ID   Q68HC0      PRELIMINARY;      PRT;   247 AA.
AC   Q68HC0;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Caspase 10 splice variant G.
GN   Name=CASP10;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pingzhang W.;
RT   "Three novel isoforms of caspase family that are deficient of
RT   conservative CASP domain.";
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY690601; AAU00989.1; -.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   Pfam; PF01335; DED; 2.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS50168; DED; 2.
SQ   SEQUENCE   247 AA;  28363 MW;  52370B5AD12C4DCF CRC64;

  Query Match            15.2%;  Score 79;  DB 2;  Length 247;
  Best Local Similarity   32.7%;  Pred. No. 20;
  Matches   34;  Conservative   15;  Mismatches   39;  Indels   16;  Gaps    5;

Qy         12 VEEALDTDEKEMLLFLCRDVAIDVVP-------PNVRDLLDILRERGKLSVGD---LAEL 61
              ::  |   : | | |||    | :||        :  |: : |     ||  |   ||||
Db         27 IDSNLGVQDVENLKFLC----IGLVPNKKLEKSSSASDVFEHLLAEDLLSEEDPFFLAEL 82

Qy         62 LYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              || :|:  ||:  |   :: ||  ||     || :| |: |: |
Db         83 LYIIRQKKLLQH-LNCTKEEVE-RLLPTRQRVSLFRNLLYELSE 124


RESULT 27
Q6KF63
ID   Q6KF63      PRELIMINARY;      PRT;   455 AA.
AC   Q6KF63;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Caspase 10.
GN   Name=CASP10;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Vonarbourg C., Fischer A., Rieux-Laucat F.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Vonarbourg C.;
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the peptidase C14 family.
DR   EMBL; AJ487678; CAD32371.1; -.
DR   HSSP; P55210; 1K86.
DR   GO; GO:0030693; F:caspase activity; IEA.
DR   GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR002138; ICE_p10.
DR   InterPro; IPR001309; ICE_p20.
DR   InterPro; IPR002398; Peptidase_C14.
DR   Pfam; PF01335; DED; 2.
DR   PRINTS; PR00376; IL1BCENZYME.
DR   SMART; SM00115; CASc; 1.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS01122; CASPASE_CYS; 1.
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DR   PROSITE; PS01121; CASPASE_HIS; 1.
DR   PROSITE; PS50207; CASPASE_P10; 1.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
KW   Hydrolase; Protease; Thiol protease; Zymogen.
SQ   SEQUENCE   455 AA;  51784 MW;  8E737FC3EC173616 CRC64;

  Query Match             15.2%;  Score 79;  DB 2;  Length 455;
  Best Local Similarity   32.7%;  Pred. No. 40;
  Matches   34;  Conservative   15;  Mismatches   39;  Indels   16;  Gaps    5;

Qy         12 VEEALDTDEKEMLLFLCRDVAIDVVP-------PNVRDLLDILRERGKLSVGD---LAEL 61
              ::  |   : | | |||    | :||       :  |: : |     ||  |   ||||
Db         27 IDSNLGVQDVENLKFLC----IGLVPNKKLEKSSSASDVFEHLLAEDLLSEEDPFFLAEL 82

Qy         62 LYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              || :|:  ||:  |   :: ||  ||     || :| |: |: |
Db         83 LYIIRQKKLLQH-LNCTKEEVE-RLLPTRQRVSLFRNLLYELSE 124


RESULT 28
Q6KF62
ID   Q6KF62      PRELIMINARY;      PRT;   478 AA.
AC   Q6KF62;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Caspase 10.
GN   Name=CASP10;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Vonarbourg C., Fischer A., Rieux-Laucat F.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Vonarbourg C.;
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the peptidase C14 family.
DR   EMBL; AJ487679; CAD32372.1; -.
DR   HSSP; P55210; 1K88.
DR   GO; GO:0030693; F:caspase activity; IEA.
DR   GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR002138; ICE_p10.
DR   InterPro; IPR001309; ICE_p20.
DR   InterPro; IPR002398; Peptidase_C14.
DR   Pfam; PF01335; DED; 2.
DR   PRINTS; PR00376; IL1BCENZYME.
DR   SMART; SM00115; CASc; 1.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS01122; CASPASE_CYS; 1.
DR   PROSITE; PS01121; CASPASE_HIS; 1.
DR   PROSITE; PS50207; CASPASE_P10; 1.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
KW   Hydrolase; Protease; Thiol protease; Zymogen.
SQ   SEQUENCE   478 AA;  54522 MW;  E78035535F8EF57B CRC64;

  Query Match             15.2%;  Score 79;  DB 2;  Length 478;
  Best Local Similarity   32.7%;  Pred. No. 42;
  Matches   34;  Conservative   15;  Mismatches   39;  Indels   16;  Gaps    5;

Qy         12 VEEALDTDEKEMLLFLCRDVAIDVVP-------PNVRDLLDILRERGKLSVGD---LAEL 61
              ::  |   : | | |||    | :||       :  |: : |     ||  |   ||||
Db         27 IDSNLGVQDVENLKFLC----IGLVPNKKLEKSSSASDVFEHLLAEDLLSEEDPFFLAEL 82

Qy         62 LYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              || :|:  ||:  |   :: ||  ||     || :| |: |: |
Db         83 LYIIRQKKLLQH-LNCTKEEVE-RLLPTRQRVSLFRNLLYELSE 124


RESULT 29
ICEA_HUMAN
ID   ICEA_HUMAN     STANDARD;      PRT;   521 AA.
AC   Q92851; Q8WYQ8; Q99845; Q9Y2U6; Q9Y2U7;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Caspase-10 precursor (EC 3.4.22.-) (CASP-10) (ICE-like apoptotic
DE   protease 4) (Apoptotic protease Mch-4) (FAS-associated death domain
DE   protein interleukin-1B-converting enzyme 2) (FLICE2).
GN   Name=CASP10; Synonyms=MCH4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM A).
RC   TISSUE=T-cell;
RX   MEDLINE=96353838; PubMed=8755496; DOI=10.1073/pnas.93.15.7464;
RA   Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA   Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA   Litwack G., Alnemri E.S.;
RT   "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT   apoptotic cysteine protease containing two FADD-like domains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM B).
RX   MEDLINE=97197836; PubMed=9045686; DOI=10.1074/jbc.272.10.6578;
RA   Vincenz C., Dixit V.M.;
RT   "Fas-associated death domain protein interleukin-1beta-converting
RT   enzyme 2 (FLICE2), an ICE/Ced-3 homologue, is proximally involved in
RT   CD95- and p55-mediated death signaling.";
RL   J. Biol. Chem. 272:6578-6583(1997).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS B AND C), AND VARIANT ILE-410.
RC   TISSUE=Spleen, and Thymus;
RX   MEDLINE=99214592; PubMed=10187817; DOI=10.1074/jbc.274.15.10301;
RA   Ng P.W., Porter A.G., Janicke R.U.;
RT   "Molecular cloning and characterization of two novel pro-apoptotic
RT   isoforms of caspase-10.";
RL   J. Biol. Chem. 274:10301-10308(1999).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX   MEDLINE=21100893; PubMed=11161814; DOI=10.1006/geno.2000.6392;
RA   Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
RA   Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA   Ikeda J.-E., Hayden M.R.;
RT   "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
RT   and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RT   critical region at chromosome 2q33-q34: candidate genes for ALS2.";
RL   Genomics 71:200-213(2001).
RN   [5]
RP   PARTIAL SEQUENCE, AND PROCESSING.
RX   MEDLINE=97121412; PubMed=8962078; DOI=10.1073/pnas.93.25.14486;
RA   Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RA   Alnemri E.S.;
RT   "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
RT   protease Mch5 is a CrmA-inhibitable protease that activates multiple
RT   Ced-3/ICE-like cysteine proteases.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
RN   [6]
RP   SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX   PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA   Hillman R.T., Green R.E., Brenner S.E.;

Qy         12 VEEALDTDEKEMLLFLCRDVAIDVVP-------PNVRDLLDILRERGKLSVGD---LAEL 61
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Db         27 IDSNLGVQDVENLKFLC----IGLVPNKKLEKSSSASDVFEHLLAEDLLSEEDPFFLAEL 82

Qy         62 LYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              || :|:  ||:  |   :: ||  ||     || :| |: |: |
Db         83 LYIIRQKKLLQH-LNCTKEEVE-RLLPTRQRVSLFRNLLYELSE 124
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RT   "An unappreciated role for RNA surveillance.";
RL   Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
RN   [7]
RP   VARIANT ALPS2 PHE-285, AND VARIANT ILE-410.
RX   MEDLINE=99339325; PubMed=10412980; DOI=10.1016/S0092-8674(00)80605-4;
RA   Wang J., Zheng L., Lobito A., Chan F.K., Dale J., Sneller M., Yao X.,
RA   Puck J.M., Straus S.E., Lenardo M.J.;
RT   "Inherited human caspase 10 mutations underlie defective lymphocyte
RT   and dendritic cell apoptosis in autoimmune lymphoproliferative
RT   syndrome type II.";
RL   Cell 98:47-58(1999).
CC   -!- FUNCTION: Involved in the activation cascade of caspases
CC       responsible for apoptosis execution. Recruited to both Fas- and
CC       TNFR-1 receptors in a FADD dependent manner. May participate in
CC       the granzyme B apoptotic pathways. Cleaves and activates caspase-
CC       3, -4, -6, -7, -8, and -9. Hydrolyzes the small- molecule
CC       substrates, Tyr-Val-Ala-Asp-|-AMC and Asp-Glu-Val-Asp-|-AMC.
CC   -!- FUNCTION: Isoform C is proteolytically inactive.
CC   -!- SUBUNIT: Heterodimer of a 23/17 kDa (p23/17) depending on the
CC       splicing events and a 12 kDa (p12) subunit.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=A; Synonyms=10-A;
CC         IsoId=Q92851-1; Sequence=Displayed;
CC       Name=B; Synonyms=10-B;
CC         IsoId=Q92851-2; Sequence=VSP_000819, VSP_000820;
CC         Note=May be produced at very low levels due to a premature stop
CC         codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC       Name=C; Synonyms=10-C;
CC         IsoId=Q92851-3; Sequence=VSP_000821, VSP_000822;
CC         Note=May be produced at very low levels due to a premature stop
CC         codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC   -!- TISSUE SPECIFICITY: Detectable in most tissues. Lowest expression
CC       is seen in brain, kidney, prostate, testis and colon.
CC   -!- PTM: Cleavage by granzyme B and autocatalytic activity generate
CC       the two active subunits.
CC   -!- DISEASE: Defects in CASP10 are the cause of type II autoimmune
CC       lymphoproliferative syndrome (ALPS2) [MIM:603909]. ALPS2 is
CC       characterized by abnormal lymphocyte and dendritic cell
CC       homeostasis and immune regulatory defects.
CC   -!- SIMILARITY: Belongs to the peptidase C14 family.
CC   -!- SIMILARITY: Contains 2 death effector (DED) domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U60519; AAC50644.1; -.
DR   EMBL; U86214; AAB46730.1; -.
DR   EMBL; AF111344; AAD28402.1; -.
DR   EMBL; AF111345; AAD28403.1; -.
DR   EMBL; AB038978; BAB32553.1; -.
DR   EMBL; AB038973; BAB32553.1; JOINED.
DR   EMBL; AB038974; BAB32553.1; JOINED.
DR   EMBL; AB038975; BAB32553.1; JOINED.
DR   EMBL; AB038977; BAB32553.1; JOINED.
DR   EMBL; AB038979; BAB32554.1; -.
DR   EMBL; AB038973; BAB32554.1; JOINED.
DR   EMBL; AB038974; BAB32554.1; JOINED.
DR   EMBL; AB038975; BAB32554.1; JOINED.
DR   EMBL; AB038976; BAB32554.1; JOINED.
DR   EMBL; AB038977; BAB32554.1; JOINED.
DR   HSSP; Q9C0K4; 1QTN.
DR   MEROPS; C14.011; -.
DR   Genew; HGNC:1500; CASP10.
DR   MIM; 601762; -.
DR   MIM; 603909; -.
DR   GO; GO:0030693; F:caspase activity; TAS.
DR   GO; GO:0006917; P:induction of apoptosis; TAS.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR002138; ICE_p10.
DR   InterPro; IPR001309; ICE_p20.
DR   InterPro; IPR002398; Peptidase_C14.
DR   Pfam; PF01335; DED; 2.
DR   Pfam; PF00656; Peptidase_C14; 1.
DR   PRINTS; PR00376; IL1BCENZYME.
DR   PROSITE; PS01122; CASPASE_CYS; 1.
DR   PROSITE; PS01121; CASPASE_HIS; 1.
DR   PROSITE; PS50207; CASPASE_P10; 1.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
KW   Alternative splicing; Apoptosis; Direct protein sequencing;
KW   Disease mutation; Hydrolase; Polymorphism; Repeat; Thiol protease;
KW   Zymogen.
FT   PROPEP        1    219
FT   CHAIN       220    415       Caspase-10 subunit p23/17.
FT   CHAIN       416    521       Caspase-10 subunit p12.
FT   DOMAIN       19     97       DED 1.
FT   DOMAIN      114    187       DED 2.
FT   ACT_SITE    358    358       By similarity.
FT   ACT_SITE    401    401       By similarity.
FT   VARSPLIC    229    271       Missing (in isoform B).
FT                                /FTId=VSP_000819.
FT   VARSPLIC    473    521       MLKFLEKTMEIRGRKRTVWGAKQISATSLPTAISAQTPRPP
FT                                MRRWSSVS -> HEDILSILTAVNDDVSRRVDKQGTKKQMP
FT                                QPAFTLRKKLVFPVPLDALSI (in isoform B).
FT                                /FTId=VSP_000820.
FT   VARSPLIC    241    273       GNRATNGAPSLVSRGMQGASANTLNSETSTKRA -> EGSC
FT                                VQDESEPQRPLCHCQQPQLYLPEGQTRNP (in isoform
FT                                C).
FT                                /FTId=VSP_000821.
FT   VARSPLIC    274    521       Missing (in isoform C).
FT                                /FTId=VSP_000822.
FT   VARIANT     285    285       L -> F (in ALPS2).
FT                                /FTId=VAR_014071.
FT   VARIANT     410    410       V -> I.
FT                                /FTId=VAR_014072.
FT   CONFLICT     68     68       E -> G (in Ref. 2).
FT   CONFLICT    268    268       T -> A (in Ref. 3).
SQ   SEQUENCE   521 AA;  58950 MW;  840348AE602B8243 CRC64;

  Query Match             15.2%;  Score 79;  DB 1;  Length 521;
  Best Local Similarity   32.7%;  Pred. No. 46;
  Matches   34;  Conservative   15;  Mismatches   39;  Indels   16;  Gaps    5;

Qy         12 VEEALDTDEKEMLLFLCRDVAIDVVP-------PNVRDLLDILRERGKLSVGD---LAEL 61
              ::  |   : | | |||    | :||       :  |: : |    ||  |   ||||
Db         27 IDSNLGVQDVENLKFLC----IGLVPNKKLEKSSSASDVFEHLLAEDLLSEEDPFFLAEL 82

Qy         62 LYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              || :|:  ||:  |   :: ||  ||     || :| |: |: |
Db         83 LYIIRQKKLLQH-LNCTKEEVE-RLLPTRQRVSLFRNLLYELSE 124


RESULT 30
Q8IUP5
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AC   Q8IUP5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CASP10 protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the peptidase C14 family.
DR   EMBL; BC042844; AAH42844.1; -.
DR   HSSP; Q9C0K4; 1QTN.
DR   GO; GO:0030693; F:caspase activity; IEA.
DR   GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   InterPro; IPR002138; ICE_p10.
DR   InterPro; IPR001309; ICE_p20.
DR   InterPro; IPR002398; Peptidase_C14.
DR   Pfam; PF01335; DED; 2.
DR   PRINTS; PR00376; IL1BCENZYME.
DR   SMART; SM00115; CASc; 1.
DR   SMART; SM00031; DED; 2.
DR   PROSITE; PS01122; CASPASE_CYS; 1.
DR   PROSITE; PS01121; CASPASE_HIS; 1.
DR   PROSITE; PS50207; CASPASE_P10; 1.
DR   PROSITE; PS50208; CASPASE_P20; 1.
DR   PROSITE; PS50168; DED; 2.
KW   Hydrolase; Protease; Thiol protease; Zymogen.
SQ   SEQUENCE   522 AA;  58993 MW;  34847E07B3DFA688 CRC64;

  Query Match             15.2%;  Score 79;  DB 2;  Length 522;
  Best Local Similarity   32.7%;  Pred. No. 46;
  Matches   34;  Conservative   15;  Mismatches   39;  Indels   16;  Gaps    5;

Qy         12 VEEALDTDEKEMLLFLCRDVAIDVVP-------PNVRDLLDILRERGKLSVGD---LAEL 61
              ::  |   : | | |||    | :||        :  |: : |     ||  |   ||||
Db         27 IDSNLGVQDVENLKFLC----IGLVPNKKLEKSSSASDVFEHLLAEDLLSEEDPFFLAEL 82

Qy         62 LYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
              || :|:  ||:  |   :: ||  ||     || :| |: |: |
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Search completed: September 30, 2005, 08:01:57
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